

SEQUENCE LISTING

<110> Genentech, Inc.
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<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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<140> 09/665,350
<141> 2000-09-18

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<151> 2000-02-22

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<151> 1999-07-07

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<212> PRT

<213> Homo sapiens

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 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
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 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
 195 200 205
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
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 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
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 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
 245 250 255
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
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 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
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 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
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 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
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 <212> DNA
 <213> Homo sapiens

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<211> 379

<212> PRT

<213> Homo sapiens

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
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Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
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Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu			
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Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
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Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
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Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His			
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Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys			
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Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
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Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
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Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
275	280		285
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu			
290	295	300	
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys			
305	310	315	320
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His			
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Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala			
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Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
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<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 8

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49

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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22

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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23

<210> 11
<211> 2197
<212> DNA
<213> Homo sapiens

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<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

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Pro	Gly	Leu	His	Leu	Arg	Gly	Ile	Arg	Asp	Ala	Gly	Gly	Arg	Tyr	Cys
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Gln	Glu	Gln	Asp	Leu	Cys	Cys	Arg	Gly	Arg	Ala	Asp	Asp	Cys	Ala	Leu
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Pro	Tyr	Leu	Gly	Ala	Ile	Cys	Tyr	Cys	Asp	Leu	Phe	Cys	Asn	Arg	Thr
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Pro	Pro	Phe	Pro	Ile	Gln	Gly	Cys	Met	His	Gly	Gly	Arg	Ile	Tyr
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Pro	Val	Leu	Gly	Thr	Tyr	Trp	Asp	Asn	Cys	Asn	Arg	Cys	Thr	Cys	Gln
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Glu	Asn	Arg	Gln	Trp	His	Gly	Gly	Ser	Arg	His	Asp	Gln	Ser	His	Gln
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Pro	Gly	Gln	Leu	Trp	Leu	Ala	Gly	Trp	Glu	Pro	Gln	Arg	Leu	Leu	Gly
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His	Asp	Pro	Gly
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<212> DNA
<213> Homo sapiens

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<223> a, t, c or g

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<210> 14
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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24

<210> 15

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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22

<210> 16

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<212> DNA

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

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 ccgtgggtgc ccccgaccc agcaggggac aggactcag gagggccag taaaggctga 780
 gatgaagtgg actgagtaga actggaggac aagagtgcac gtgagttctt gggagtctcc 840
 agagatgggg cctggaggcc tggaggaagg ggccaggct cacattcgtg gggctccctg 900
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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

Met	Thr	His	Arg	Thr	Thr	Trp	Ala	Arg	Arg	Thr	Ser	Arg	Ala	Val
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Thr	Pro	Thr	Cys	Ala	Thr	Pro	Ala	Gly	Pro	Met	Pro	Cys	Ser	Arg	Leu
			20					25					30		

Pro	Pro	Ser	Leu	Arg	Cys	Ser	Leu	His	Ser	Ala	Cys	Cys	Ser	Gly	Asp
			35				40					45			

Pro	Ala	Ser	Tyr	Arg	Leu	Trp	Gly	Ala	Pro	Leu	Gln	Pro	Thr	Leu	Gly
			50			55					60				

Val	Val	Pro	Gln	Ala	Ser	Val	Pro	Leu	Leu	Thr	Asp	Leu	Ala	Gln	Trp
65						70				75				80	

Glu	Pro	Val	Leu	Val	Pro	Glu	Ala	His	Pro	Asn	Ala	Ser	Leu	Thr	Met
			85					90				95			

Tyr	Val	Cys	Thr	Pro	Val	Pro	His	Pro	Asp	Pro	Pro	Met	Ala	Leu	Ser
			100				105					110			

Arg	Thr	Pro	Thr	Arg	Gln	Ile	Ser	Ser	Asp	Thr	Asp	Pro	Pro	Ala
115						120				125				

Asp	Gly	Pro	Ser	Asn	Pro	Leu	Cys	Cys	Cys	Phe	His	Gly	Pro	Ala	Phe
130						135				140					

Ser	Thr	Leu	Asn	Pro	Val	Leu	Arg	His	Leu	Phe	Pro	Gln	Glu	Ala	Phe
145						150				155			160		

Pro	Ala	His	Pro	Ile	Tyr	Asp	Leu	Ser	Gln	Val	Trp	Ser	Val	Val	Ser
					165			170				175			

Pro	Ala	Pro	Ser	Arg	Gly	Gln	Ala	Leu	Arg	Arg	Ala	Gln
						180		185				

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 19

tgctgtgcta ctcctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 20

tgcacaaggc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23

Met	Gly	Ala	Ala	Arg	Leu	Leu	Pro	Asn	Leu	Thr	Leu	Cys	Leu	Gln	Leu
1															
					5					10					15

Leu	Ile	Leu	Cys	Cys	Gln	Thr	Gln	Tyr	Val	Arg	Asp	Gln	Gly	Ala	Met
					20				25						30

Thr	Asp	Gln	Leu	Ser	Arg	Arg	Gln	Ile	Arg	Glu	Tyr	Gln	Leu	Tyr	Ser
					35				40						45

Arg	Thr	Ser	Gly	Lys	His	Val	Gln	Val	Thr	Gly	Arg	Arg	Ile	Ser	Ala
					50			55					60		

Thr	Ala	Glu	Asp	Gly	Asn	Lys	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp
					65		70			75					80

Thr	Phe	Gly	Ser	Arg	Val	Arg	Ile	Lys	Gly	Ala	Glu	Ser	Glu	Lys	Tyr
					85			90							95

Ile	Cys	Met	Asn	Lys	Arg	Gly	Lys	Leu	Ile	Gly	Lys	Pro	Ser	Gly	Lys
					100			105				110			

Ser	Lys	Asp	Cys	Val	Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr
					115		120			125					

Ala	Phe	Gln	Asn	Ala	Arg	His	Glu	Gly	Trp	Phe	Met	Ala	Phe	Thr	Arg
					130		135			140					

Gln	Gly	Arg	Pro	Arg	Gln	Ala	Ser	Arg	Ser	Arg	Gln	Asn	Gln	Arg	Glu
					145		150			155			160		

Ala	His	Phe	Ile	Lys	Arg	Leu	Tyr	Gln	Gly	Gln	Leu	Pro	Phe	Pro	Asn
					165			170			175				

His	Ala	Glu	Lys	Gln	Lys	Gln	Phe	Glu	Phe	Val	Gly	Ser	Ala	Pro	Thr
					180			185			190				

Arg	Arg	Thr	Lys	Arg	Thr	Arg	Arg	Pro	Gln	Pro	Leu	Thr			
					195		200			205					

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 24

cagtagtga gggaccaggg cgccatga

28

<210> 25

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

 <400> 25
 ccgtgacct gcacgtgctt gccca 24

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<220>
 <221> modified_base
 <222> (21)
 <223> a, t, c or g

 <400> 26
 gcggatctgc cgccctgctca nctggtcggt catggcgccc t 41

<210> 27
 <211> 2479
 <212> DNA
 <213> Homo sapiens

 <400> 27
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 ttaccatacg ccctcaggac gtccctcta gctggagttc tggacttcaa cagaacccc 180
 tccagtcatc ttgattttgc tggttatttt ttttttctt ttctttttcc caccacattg 240
 tattttattt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300
 ctttttctt gaagtcttgg ctatcattt ccctgggct ctactcacag gtgtccaaac 360
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 gcttgacctc agtgcctctt ggatcccgg agggcgtaac cgtactctac ctccacaaca 480
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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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1															15

5

10

Lys	Ser	Trp	Leu	Ile	Ile	Ser	Leu	Gly	Leu	Tyr	Ser	Gln	Val	Ser.	Lys
															30

20

25

30

Leu	Leu	Ala	Cys	Pro	Ser	Val	Cys	Arg	Cys	Asp	Arg	Asn	Phe	Val	Tyr
															45

35

40

45

Cys	Asn	Glu	Arg	Ser	Leu	Thr	Ser	Val	Pro	Leu	Gly	Ile	Pro	Glu	Gly
															50

50

55

60

Val	Thr	Val	Leu	Tyr	Leu	His	Asn	Asn	Gln	Ile	Asn	Asn	Ala	Gly	Phe
															65

65

70

80

Pro	Ala	Glu	Leu	His	Asn	Val	Gln	Ser	Val	His	Thr	Val	Tyr	Leu	Tyr
															85

85

90

95

Gly	Asn	Gln	Leu	Asp	Glu	Phe	Pro	Met	Asn	Leu	Pro	Lys	Asn	Val	Arg
															100

100

105

110

Val	Leu	His	Leu	Gln	Glu	Asn	Asn	Ile	Gln	Thr	Ile	Ser	Arg	Ala	Ala
															115

115

120

125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
 275 280 285
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
 290 295 300
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
 305 310 315 320
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
 325 330 335
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
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 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
 370 375 380
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
 385 390 395 400
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405

410

415

Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val
 420 425 430

Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met
 435 440 445

Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly
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Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu
 465 470 475 480

Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu
 485 490 495

Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala
 500 505 510

Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser
 515 520 525

His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala
 530 535 540

Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser
 545 550 555 560

Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys
 565 570 575

Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly
 580 585 590

Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln
 595 600 605

Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu
 610 615 620

Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His
 625 630 635 640

Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu
 645 650 655

His Cys His Thr
 660

<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 29

cgggtctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 30

gcaggacaac cagataaaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 32

ttcacgggct gctttgcc agctttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

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<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met	Glu	Lys	Met	Leu	Ala	Gly	Cys	Phe	Leu	Leu	Ile	Leu	Gly	Gln	Ile
1				5					10				15		

Val	Leu	Leu	Pro	Ala	Glu	Ala	Arg	Glu	Arg	Ser	Arg	Gly	Arg	Ser	Ile
				20				25				30			

Ser	Arg	Gly	Arg	His	Ala	Arg	Thr	His	Pro	Gln	Thr	Ala	Leu	Leu	Glu
				35				40				45			

Ser	Ser	Cys	Glu	Asn	Lys	Arg	Ala	Asp	Leu	Val	Phe	Ile	Ile	Asp	Ser
				50				55				60			

Ser	Arg	Ser	Val	Asn	Thr	His	Asp	Tyr	Ala	Lys	Val	Lys	Glu	Phe	Ile
				65				70			75			80	

Val	Asp	Ile	Leu	Gln	Phe	Leu	Asp	Ile	Gly	Pro	Asp	Val	Thr	Arg	Val
				85				90				95			

Gly	Leu	Leu	Gln	Tyr	Gly	Ser	Thr	Val	Lys	Asn	Glu	Phe	Ser	Leu	Lys
				100				105				110			

Thr	Phe	Lys	Arg	Lys	Ser	Glu	Val	Glu	Arg	Ala	Val	Lys	Arg	Met	Arg
				115				120				125			

His	Leu	Ser	Thr	Gly	Thr	Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Leu
				130				135				140			

Asn	Ile	Ala	Phe	Ser	Glu	Ala	Glu	Gly	Ala	Arg	Pro	Leu	Arg	Glu	Asn
				145				150			155			160	

Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser
				165				170				175			

Val	Ala	Glu	Val	Ala	Ala	Lys	Ala	Arg	Asp	Thr	Gly	Ile	Leu	Ile	Phe
				180				185				190			

Ala	Ile	Gly	Val	Gly	Gln	Val	Asp	Phe	Asn	Thr	Leu	Lys	Ser	Ile	Gly
				195				200				205			

Ser	Glu	Pro	His	Glu	Asp	His	Val	Phe	Leu	Val	Ala	Asn	Phe	Ser	Gln
				210				215				220			

Ile	Glu	Thr	Leu	Thr	Ser	Val	Phe	Gln	Lys	Lys	Leu	Cys	Thr	Ala	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245	250		255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260	265		270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275	280		285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290	295		300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305	310	315	320
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325	330		335
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340	345		350
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355	360		365
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370	375		380
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385	390	395	400
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405	410		415
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420	425		430
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435	440		445
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450	455		460
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465	470	475	480
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485	490		495
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500	505		510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525

Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540

Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560

Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575

Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590

Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605

Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620

Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640

Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
 645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700

Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735

Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750

Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
 885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
 900 905 910

Arg Tyr Arg
 915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 36

acagccatgg tctatacgctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

ggagccgccc tgggtgtcag cggctcggtc cccgcgcacg ctccggccgt cgcgacgcct 60
 cggcacctgc aggtccgtgc gtccccggc tggcccccct gactccgtcc cggccaggga 120
 gggccatgtat ttccctcccg ggccccctgg tgaccaactt gctcggttt ttgttccctgg 180
 ggctgagtgc cctcgccccc ccctcgccgg cccagctgca actgcacttg cccggcaacc 240
 gggtgcaggc ggtggaggga gggaaagtgg tgcttccagc gtggtagcacc ttgcacgggg 300
 aggtgtcttc atcccccca tgggaggtgc cctttgtat gtgggtttc aaacagaaaag 360
 aaaaggagga tcagggtttc tccatcatca atggggtcac aacaagaaa cctggagtt 420
 ctttgtcta ctccatggcc tcccgaaacc tgcctcgcg gctggagggt ctccaggaga 480
 aagactctgg cccctacagc tgctccgtga atgtcaaga caaacaaggc aaatctaggg 540
 gccacagcat caaaacctta gaactcaatg tactgttcc tccagctctt ccatccgtcc 600
 gtctccaggc tggcccat gtggggggcaa acgtgaccct gagctgccag ttcataaggaa 660
 gtaagccgc tggccatatac cagtgggatc ggcagttcc atccttccag acttttttg 720
 caccagcatt agatgtcatc cgtgggtctt taagcctcac caaccttcc tttccatgg 780
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 ataacctgtc aggctggctt gtttaggttt tactggggca gaggataggg aatctttat 1740
 taaaactaac atgaaatatg tgggttttc atttgcataat taaaataaag atacataatg 1800
 tttgtatgaa aaa 1813

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln			
20	25	30	
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val			
35	40	45	
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln			
50	55	60	
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys			
65	70	75	80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro			
85	90	95	
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg			
100	105	110	
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val			
115	120	125	
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
145	150	155	160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
165	170	175	
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275	280	285	

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
 370 375 380

Gln Ala Gly Ser Leu Val
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 42
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 43
gtgtgacaca gcgtgggc 18

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 44
gaccggcagg cttctgct 18

<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 45
cagcagcttc agccaccagg agtgg 25

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 46
ctgagccgtg ggctgcagtc tcgc 24

<210> 47

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 47
ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
<211> 2822
<212> DNA
<213> Homo sapiens

<400> 48
cgccaccact gcccacccg ccaatgaaac gcctcccgct cctagtgggtt ttttccactt 60
tgttgaattt ttcctatact caaaaattgca ccaagacacc ttgtctccca aatgcaaaat 120
gtgaaatacg caatggaaattt gaagcctgct attgcaacat gggattttca ggaaatggtg 180
tcacaatttgc tgaagatgtat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240
ctaattgcac taacacagaa ggaaggattt attgtatgtg tgtacctggc ttcagatcca 300
gcagtaacca agacagggtt atcactaatg atggAACCGT ctgtatagaa aatgtgaatg 360
caaactgcca ttttagataat gtctgtatag ctgcaaataat taataaaaact ttaacaaaaa 420
tcagatccat aaaagaacct gtggcttgc tacaagaatg ctatagaaat tctgtgacag 480
atcttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540
taggttacaa gaacaacact atctcagcca aggacacccct ttctactca actcttactg 600
aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgttagtt tgggacaagt 660
tatctgtgaa tcataggaga acacatctta caaaaactcat gcacactgtt gaacaagcta 720
ctttaaggat atccccagac ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780
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aagaatatta cagattgttc aaaaatgtcc cctgttgc tggatgttta aggtaaacat 2100
agagaatgggt ggataattac aactgcacca aaataaaaaat tccaaagctgtt ggttgcacca 2160

tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtattttaa 2220
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 ggaaagtaat tggtttctca ggagtgatat cactgcaccc aaggaaagat tttcttcata 2400
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 agacttctgt ttgctaattc tggcttttt tctaatttc taaaaaaaaaaa aaaaaggttt 2760
 acctccacaa attgaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2820
 aa 2822

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

Met	Lys	Arg	Leu	Pro	Leu	Leu	Val	Val	Phe	Ser	Thr	Leu	Leu	Asn	Cys
1															15

5

10

Ser	Tyr	Thr	Gln	Asn	Cys	Thr	Lys	Thr	Pro	Cys	Leu	Pro	Asn	Ala	Lys
															30

20

25

Cys	Glu	Ile	Arg	Asn	Gly	Ile	Glu	Ala	Cys	Tyr	Cys	Asn	Met	Gly	Phe
															45

35

40

45

Ser	Gly	Asn	Gly	Val	Thr	Ile	Cys	Glu	Asp	Asp	Asn	Glu	Cys	Gly	Asn
															60

50

55

60

Leu	Thr	Gln	Ser	Cys	Gly	Glu	Asn	Ala	Asn	Cys	Thr	Asn	Thr	Glu	Gly
															80

65

70

75

80

Ser	Tyr	Tyr	Cys	Met	Cys	Val	Pro	Gly	Phe	Arg	Ser	Ser	Ser	Asn	Gln
															95

85

90

95

Asp	Arg	Phe	Ile	Thr	Asn	Asp	Gly	Thr	Val	Cys	Ile	Glu	Asn	Val	Asn
															110

100

105

110

Ala	Asn	Cys	His	Leu	Asp	Asn	Val	Cys	Ile	Ala	Ala	Asn	Ile	Asn	Lys
															125

115

120

125

Thr	Leu	Thr	Lys	Ile	Arg	Ser	Ile	Lys	Glu	Pro	Val	Ala	Leu	Leu	Gln
															130

130

135

140

Glu	Val	Tyr	Arg	Asn	Ser	Val	Thr	Asp	Leu	Ser	Pro	Thr	Asp	Ile	Ile
															145

150

155

160

Thr	Tyr	Ile	Glu	Ile	Leu	Ala	Glu	Ser	Ser	Ser	Leu	Leu	Gly	Tyr	Lys
															165

165

170

175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
 675 680 685

Leu Arg
 690

<210> 50
 <211> 589
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (61)

<223> a, t, c or g

<400> 50

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 ngaaaagccg gcatatggat tcaaattggca atgttcagt tgcatttttta tattataaga 120
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 52

ggagtagaaa ggcgcattgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 55

ggatctcctg agtcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 56

cctagtttag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcgggtggga ggagttcccc gaaacccggc 60
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gggacaaga ggcgcccgcct gcctggccgg gccccgggag ggggctgggg ctggggccgg 180
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gaacccttcc cccagcactt ggtttccaa catgatattt atgagtaatt tattttgata 2040
tgtacatctc ttatttctt acattattta tgcccccaaa ttatattat gtatgtaaat 2100
gaggttggtt ttgtatatta aaatggagtt tgtttgt 2137

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
 115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
 130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
 145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
 165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
 195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 60

atccgccccag atggctacaa tgtgtta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 61

gcctcccggt ctcccgtgagc agtgccaaac agcggcagtg ta

42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 62
 ccagtccggc gacaagcccc aa

22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
 cccagaagtt caaggcccc cggcctcctg cgctcctgcc gcccggaccc tcgacccct 60
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 gctgctgctg cgctacctgg tggtcgccct gggctatcat aaggcctatg gttttctgc 180
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctatt tagcctgcaa 240
 aaccccaaag aagactgtt cctccagatt agagtggaaag aaactgggtc ggagtgtctc 300
 ctttgtctac tatcaacaga ctcttcagg tgatttaaa atcggatctg agatgataga 360
 tttcaatatac cggataaaa atgtgacaag aagtgtatgc gggaaatatac gttgtgaagt 420
 tagtgccccca tctgagcaag gcacaaaacct ggaagaggat acagtcaactc tggaagtatt 480
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 aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720
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<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr
 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Asp Thr Val Thr Leu
 115 120 125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240

Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270

Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
 290 295 300

Gly Gly Ser Arg Gly Gln Glu Phe

305	310	
<p><210> 65 <211> 22 <212> DNA <213> Artificial Sequence</p>		
<p><220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe</p>		
<p><400> 65 atcgttgtga agtttagtgcc cc 22</p>		
<p><210> 66 <211> 23 <212> DNA <213> Artificial Sequence</p>		
<p><220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe</p>		
<p><400> 66 acctgcgata tccaaacagaa ttg 23</p>		
<p><210> 67 <211> 48 <212> DNA <213> Artificial Sequence</p>		
<p><220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe</p>		
<p><400> 67 ggaagaggat acagtcaactc tggaagtatt agtggctcca gcagttcc 48</p>		
<p><210> 68 <211> 2639 <212> DNA <213> Homo sapiens</p>		
<p><400> 68 gacatcgag gtgggctagc actgaaaactg ctttcaaga cgaggaagag gaggagaaag 60 agaaaagaaga ggaagatgtt gggcaacatt tatttaacat gctccacagc ccggaccctg 120 gcatcatgct gctattccctg caaatactga agaaggcatgg gatttaataa ttttacttct 180 aaataaaatga attactcaat ctccatgac catctataca tactccacct tcaaaaagta 240 catcaatatt atatcattaa ggaaatagta accttctctt ctccaaatatg catgacattt 300 ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtggttcta 360 tggcattcat catttgacaa atgcaagcat cttccatttac aatcagctcc tattgaactt 420 actagcactg actgtgaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagta 540</p>		

aagctgtaga taaaaaaagtg gattgtccac ggatatgtac gtgtgaaatc aggccttgg 600
ttacaccagg atccatttat atggaagcat ctacagtggta ttgtaatgat ttaggtcttt 660
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<210> 69
<211> 708
<212> PRT
<213> Homo sapiens

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
 20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
 35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
480		
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
560		
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
705

<210> 70
<211> 1305
<212> DNA
<213> Homo sapiens

<400> 70
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ttaccacgt tggtagtggat gatgagaaat gggctcgta ttatgctgac attccagcat 180
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gtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720
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cccccttaa ttgtacccccc gatggatata ttctgagtaa gctactatct gaacatttagt 1200
tagatccatc tcactattta ataatgaaat ttattttttt aattaaaag caaataaaag 1260
cttaactttt aaccatggaa aaaaaaaaaaa aaaaaaaaaaa aaaca 1305

<210> 71
<211> 259
<212> PRT
<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu			
1	5	10	15
Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser			
20	25	30	
Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val			
35	40	45	
Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro			
50	55	60	
Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro			
65	70	75	80
Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser			
85	90	95	
Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala			
100	105	110	
Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val			
115	120	125	
His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn			
130	135	140	
Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met			
145	150	155	160
Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val			
165	170	175	
Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala			
180	185	190	
Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val			
195	200	205	
Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr			
210	215	220	
Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys			
225	230	235	240
Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser			
245	250	255	
Thr Val Val			

<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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 tgctgggctc aytgtgtca ggctcgccca cgggctgccc gccccgctgc gagtgctccg 180
 cccaggaccg cgctgtgtcg tgccaccgca aytgtttgt ggcagtcccc gagggcatcc 240
 ccacccgagac ggcctgtcg gacctaggca agaaccgcat caaaaacgctc aaccaggacg 300
 agttcgccag ctcccccac ctggaggagc tggagctcaa cgagaacatc gtgagcgcgg 360
 tggagcccg cgcccttcaac aaccttca acctccggac gctgggtctc cgcaagcaacc 420
 gcctgaagct catcccgcta ggcgttca acctccgtcg caacctgacc aagcaggaca 480
 tcagcgagaa caagatcgaa atcctactgg actacatgtt tcaggacctg tacaacctca 540
 agtcacttggaa ggttggcgac aatgacactcg tctacatctc tcaccgcgcc tttagcggcc 600
 tcaacagcct ggagcagctg acgctggaga aatgcaacatc gacctccatc cccaccggagg 660
 cgctgtccca cctgcacggc ctcatcgatc tgaggctccg gcacctcaac atcaatgcca 720
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 cctacttggaa caccatgaca cccaaactgccc tctacggcct caacctgacg tccctgtcca 840
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 aaaaaaaaaa 2290

<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Val Leu Gly
 20 25 30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
 305 310 315 320

 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
 325 330 335

 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
 340 345 350

 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
 355 360 365

 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380

 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400

 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415

 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430

 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445

 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460

 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480

 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495

 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510

 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525

 Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540

 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560

 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575

 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser		
595	600	605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile		
610	615	620

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 74

tcacacctggag cctttattgg cc

22

<210> 75

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 75

ataccaggcta taaccaggct gcg

23

<210> 76

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg
gg

50

52

<210> 77

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 77	
ccatgtgtct cctcctacaa ag	22
<210> 78	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 78	
ggaaatagat gtgatctgat tgg	23
<210> 79	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 79	
cacctgttagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg	50
<210> 80	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 80	
agcaaccgcc tgaagctcat cc	22
<210> 81	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 81	
aaggcgccgt gaaaatgt aacg	24
<210> 82	

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 82
 gactacatgt ttcaggacct gtacaacctc aagtcaactgg aggttggcga 50

<210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<400> 83
 cccacgcgtc cgcacccctcgcc cccccgggctc cgaagcggct cggggggcgcc ctttcggtca 60
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 agccaggagg cccggccggga agcgcgatgg gggcccccagc cgcctcgctc ctgtctctgc 180
 tcctgtctttt cgcctcgctc tgccgcggcc gggggccaa cctctcccaag gacgacagcc 240
 agccctggac atctgtatgaa acagtgggtgg ctgggtggcac cgtgggtgtc aagtgc当地 300
 tggaaatgtca cgaggactca tccctgcaat ggtctaaccct tgctcagcag actctctact 360
 ttggggagaaa gagagccctt cgagataatc gaattcagct gtttacctt acgc当地ccacagc 420
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 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Phe Ala
 1 5 10 15

Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
 . 20 . 25 . 30 .

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp.
 65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly.
 115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
 305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 85

gcttaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 86

aaccttggaaat gtcaccggagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87	
cctagcacag tgacgaggga cttggc	26
<210> 88	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 88	
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc	50
<210> 89	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 89	
gccctggcag acgagggcga gtacacctgc tcaatttca ctatgcctgt	50
<210> 90	
<211> 2755	
<212> DNA	
<213> Homo sapiens	
<400> 90	
gggggttagg gaggaaggaa tccaccccca ccccccaaaa ccctttctt ctccttcct 60	
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 tacccaaattc cccgcctcat cagcctggat gggcataagt agataaataa ctgtgagctc 2400
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

Met	Leu	Leu	Trp	Ile	Leu	Leu	Glu	Thr	Ser	Leu	Cys	Phe	Ala	Ala
1														

5

10

15

Gly	Asn	Val	Thr	Gly	Asp	Val	Cys	Lys	Glu	Lys	Ile	Cys	Ser	Cys	Asn

20

25

30

Glu	Ile	Glu	Gly	Asp	Leu	His	Val	Asp	Cys	Glu	Lys	Lys	Gly	Phe	Thr

35

40

45

Ser	Leu	Gln	Arg	Phe	Thr	Ala	Pro	Thr	Ser	Gln	Phe	Tyr	His	Leu	Phe

50

55

60

Leu	His	Gly	Asn	Ser	Leu	Thr	Arg	Leu	Phe	Pro	Asn	Glu	Phe	Ala	Asn

65

70

75

80

Phe	Tyr	Asn	Ala	Val	Ser	Leu	His	Met	Glu	Asn	Asn	Gly	Leu	His	Glu

85

90

95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
 100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190

Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205

Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220

Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240

Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270

Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285

Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
 290 295 300

Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
 305 310 315 320

Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335

Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
 340 345 350

Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365

Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
 385 390 395 400

Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn
 405 410 415

Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser
 420 425 430

Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn
 435 440 445

Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro
 450 455 460

Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
 465 470 475 480

Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu
 485 490 495

Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
 500 505 510

Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
 515 520 525

Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
 530 535 540

Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560

Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
 565 570 575

Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
 580 585 590

Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
 595 600 605

Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu
 610 615 620

Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
 625 630 635 640

Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
 645 650 655

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660

665

670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp
 675 680 685

Cys Gly Ser His Ser Leu Ser Asp
 690 695

<210> 92

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 92

gttggatctg ggcaacaata ac

22

<210> 93

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 93

attgttgtgc aggctgagtt taag

24

<210> 94

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 94

ggtggtata catggatagc aattacctgg acacgctgtc ccgggg

45

<210> 95

<211> 2226

<212> DNA

<213> Homo sapiens

<400> 95

agtgcactgc gtcccctgta cccggcgcca gctgtgttcc tgaccccaga ataaactcagg 60
 gctgcacccgg gcctggcagc gtcggcaca catttcctgt cgccggcctaa gggaaactgt 120
 tggccgctgg gccccggggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

gaggggaaagg gagggggaaac cgggttgggg aagccagctg tagagggcggt tgaccgcgtc 240
ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300
ggggcctcag agaatgaggc cggcgttcgc cctgtccctc ctctggcagg cgctctggcc 360
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aatttacatt aaaaaataat ttctacccaaa atggaaagga aatgttctat gttgttcagg 2160
ctaggagtat attggttcga aatcccaggg aaaaaaataa aaataaaaaaa taaaaggatt 2220
gttcat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
1 5 10 15

Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly			
65	70	75	80
Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu			
85	90	95	
Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly			
100	105	110	
Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu			
115	120	125	
Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala			
130	135	140	
Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met			
145	150	155	160
Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu			
165	170	175	
Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr			
180	185	190	
Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro			
195	200	205	
Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val			
210	215	220	
Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly			
225	230	235	240
Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys			
245	250	255	
Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu			
260	265	270	
Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr			
275	280	285	
Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg			
290	295	300	
Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro			
305	310	315	320
Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln			
325	330	335	
Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln			

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	
<210> 97		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 97		
tggaaaggaga tgcgatgccca cctg		24
<210> 98		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 98		
tgaccagtgg ggaaggacag		20

<210> 99
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 99
 acagagcaga gggtgccctg 20

<210> 100
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 100
 tcagggacaa gtggtgtctc tccc 24

<210> 101
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 101
 tcagggaagg agtgtgcagt tctg 24

<210> 102
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 102
 acagctccccg atctcagtta ctgcgcggc ggacgaaatc ggcgctcgct 50

<210> 103
 <211> 2026
 <212> DNA
 <213> Homo sapiens

<400> 103

cgacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca gggaaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgcctt gccggccg 120
tatccccgg ctacctggc cgccccggg cggtgcgcg gtgagagggg ggcgcggg 180
agccgagcgc cggtgtgac cagcgtctgtt gccagtgtg gccgggggtg gagcgcgtg 240
ggtcggagg ggcgtgtgtg ccggcgccg cgcgtgggg tgcaaacccc gacgtctac 300
gctccatga gggcgcgaa cgcctggcg caactctgcc tgctgtggc tgccgcacc 360
cagctctcg cgcagcgtc cccagagaga cctgtttca catgtggtg cattctact 420
ggagagctg gatttattgg cagtgaaggt tttcctggag tgcacccccc aaatacgaaa 480
tgtacttggaa aatcacagt tcccaagga aagtagtgc ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgcccstat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgcgtccagt 660
ggcaacaaga tgcgtgtca gatgatttct gatgccaaca cagctggcaa tggcttcatg 720
ccatgttct ccgctgctga accaaacgaa agaggggatc agtattgtgg aggactcctt 780
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gtcaacttgc tgcgtgcacat tgcgtggggca aagaatcage ttatagaatt aaagtttag 900
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caaaaagtta gacggacggg gactctggag gcaattatt gttcaagtga ctttgttata 1260
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gtgttatttgc ttccacccatc aaggcccttgc cctgagggtt tacaatcttgc tcttgccgtt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaaa aaaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met Arg G

1

Ala Thr Glu

20 25 30

Digitized by srujanika@gmail.com

1

1

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
 50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu			
65	70	75	80
Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly			
85	90	95	
His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro			
100	105	110	
Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser			
115	120	125	
Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala			
130	135	140	
Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg			
145	150	155	160
Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro			
165	170	175	
Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu			
180	185	190	
Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys			
195	200	205	
Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala			
210	215	220	
Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val			
225	230	235	240
Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu			
245	250	255	
Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu			
260	265	270	
Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Phe Pro Val Thr Thr			
275	280	285	
Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr			
290	295	300	
Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly			
305	310	315	320
Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val			
325	330	335	
Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala			

<213> Homo sapiens

<400> 108

cgacgcgtg	ggcgacgcg	tggccggccc	acggcgcggc	cgggctgggg	cggtcgttcc	60
tcccttcgtcc	gtggcctacg	agggtccccca	gcctgggtaa	agatggcccc	atggccccc	120
aagggcctag	tcccagctgt	gctctggggc	ctcagccct	tcctcaacct	cccaggac	180
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catacctgcc	ggggactgg	tgacagcttt	aacaaggccc	tggagagaac	catccgggac	300
aactttggag	gtggaaacac	tgcctgggag	gaagagaatt	tgtccaaata	caaagacagt	360
gagaccgc	tggtagaggt	gctggaggg	gtgtgcagca	agtcaagactt	cgagtgccac	420
gcgcctgtgg	agctgagtga	ggagctgg	gagagctgt	ggttcacaa	gcagcaggag	480
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gataccatga	gctttcacc	tggcgggac	tggcagg	cacaatgt	gaatttcaaa	1620
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acaggggtgg	ggccatcac	gtccctc	gca	tgctgca	tcctgttctg	1740
tgttcaccac	atccccacac	ccattgcca	tttattt	catctcagg	aataaagaaa	1800
qgtcttqaa	at	aaaaaaa	aaaaaaa	aaaaaaa		1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
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Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
50 55 60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
 65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
 85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
 100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
 115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
 130 135 140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
 145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
 165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Glu Ala Cys
 180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
 195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
 210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
 225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
 245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
 260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
 275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
 290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
 325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365

Met Phe Phe Gly Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415

Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 112

atctgcttgtt agccctcgac ac

22

<210> 113

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1461)

<223> a, t, c or g

<400> 113

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 cggggccgccc ctgaccgggg agacgtctt gggcagcctg ctgcggcagc tgcagctaa 180
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcatccccca cccacgtgag 240
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300
 cagccagagc ttccgagagg tggccggcag gttccctggcg ttggaggcca gcacacacct 360
 gctggtgttc ggcattggaga acggcgtgcc gcccaacagc gagctggtgc aggccgtgct 420
 gcggtcttc caggagccgg tcccccaaggc cgccgtgcac aggacacgggc ggctgtcccc 480
 ggcgcagcgc cgggcccggg tgaccgtcga gtggctgcgc gtccgcgacg adggctccaa 540
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 cgacgtgacc gaggccgtga acttctggca gcagctgagc cggcccccggc agccgctgct 660
 gctacaggtg tcgggtcaga gggagcatct gggcccgctg gcgtccggcg cccacaagct 720
 ggtccgcctt gcctcgcagg gggcgcgcagg cgggcttggg gagccccagc tggagctgca 780
 caccctggac cttggggact atggagctca gggcgaactgt gaccctgaag caccaatgac 840
 cgagggcacc cgctgtgcc gcaaggagat gtacattgac ctgcaggggaa tgaagtggc 900
 cgagaactgg gtgctggagc ccccgccctt cctggcttat gagttgtgtgg gcacctgccc 960
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 gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgctgat 1260
 ggacaaatgc tctgtgtct ctgtgagcc ctgaatttgc ttccctgtac aagttaatc 1320
 acctaatttt tgcttctcag gaatgagaat ctttgccac tggagagccc ttgctcagtt 1380
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 aaagtccctcc accaccactc tgacctaag acctgggtt aagtgtgggt tgcaccc 1560
 caatccagat aataaagact ttgtaaaaca tgaataaaac acatttattt ctaaaa 1616

<210> 114

<211> 366

<212> PRT

<213> Homo sapiens

<400> 114

Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala

1

5

10

15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu

20

25

30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met

35

40

45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190

Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 115

aggactgcca taacttgccct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgcgtaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtccctt cggcggttgt tttgttcagtgc gcctgatcgc gatggggaca 60
 aaggcgcaag tcgagaggaa actgttgtgc ctttcatat tggcgatcct gttgtgctcc 120
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcaaat tcctgagaat 180

aatcctgtga agttgtcctg tgccactcg ggctttctt ctcgggtgt ggagtggaaag 240
 tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agttcctat 300
 gaggaccggg tgaccttctt gcacaactggg atcacccatca agtccgtgac acggaaagac 360
 actggggacat acacttgat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
 gtcaagctca tcgtgcttgc gctccatcc aagcctacag ttaacatccc ctcccttgcc 480
 accattggga accggggcagt gtcgacatgc tcagaacaag atggttcccc accttctgaa 540
 tacacctggt tcaaagatgg gatagtatg cctacgaatc cccaaagcac ccgtgccttc 600
 agcaacttctt cctatgtctt gaatcccaca acaggagagc tggctttga tccctgtca 660
 gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
 tcaaattgtg tgcgcatgga agctgtggag cggaaatgtgg ggttcatcg ggcagccgtc 780
 cttgtAACCC tgattctctt gggaaatctt gttttggca tctgggttgc ctatagccgaa 840
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 agtggccgaa gtgaaggaga attcaaacag acctcgcat tcctgggtg agcctgggtc 960
 gtcaccggc tatcatctgc attgcctt ctcagggtc accggactt ggcggctgt 1020
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 ctctggccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
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 ggagaaaccc tactggaaat acaaagttt ccaggcatgg tggtgcatgc ctgttagtccc 1800
 agctgctcag gacctggca acaagagcaa aactccagct caaaaaaaaaa aaaaaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Leu	Cys	Leu	Phe	Ile
1									10						15

Leu	Ala	Ile	Leu	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr	Val	His
20										25				30	

Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro	Val	Lys	Leu
35									40				45		

Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val	Glu	Trp	Lys	Phe
50									55				60		

Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr
65									70				75		80

Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu	Pro	Thr	Gly	Ile	Thr	Phe
85									90				95		

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly
 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

<210> 121

<211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 121
tgatcgcgat ggggacaaag gcgcaggctc gagaggaaac tgttgtgcct 50

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 122
acacctgggtt caaagatggg 20

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 123
taggaagagt tgctgaaggc acgg 24

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 124
ttgccttact caggtgctac 20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 125
actcagcagt ggttaggaaag 20

<210> 126

<211> 1210

<212> DNA

<213> Homo sapiens

<400> 126
cagcgcgtgg ccggcgccgc tgtggggaca gcatgagcgg cggttggatg gcgcagggtt 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactag 120
gcctggaggc cgccgcgagc ccgccttcca ccccgcaccc tcgcggccgc gcaggcccc 180
gctcaggctc gtgcacccacc accaagtcc agtgccgcac cagtggtcta tgcgtgcggc 240
tcacctggcg ctgcgacagg gacttggact gcagcgtatgg cagcgtatgag gaggagtgca 300
ggattgagcc atgtacccag aaagggcaat gcccacccgc ccctggccct ccctgcggcc 360
gcacccggcgt cagtgaactgc tctggggaaa ctgacaagaa actgcgcac acgtgcgc 420
tggcctgcct agcaggcgag ctccggttgc cgcgtgcga tgactgcatt ccactcacgt 480
ggcgcgtgcga cggccacccca gactgtcccg actccagcga cgagctcgcc tggtaacca 540
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600
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gggttattgc agctgcgtcg gtgetcagtg caagcctggt caccgcaccc ctccctcc 780
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agcttaggatg gggAACCTGC cacagccaga actgagggggc tggcccccagg cagctccc 1140
gggtagaaac gcccctgtgc ttaagacact ccctgcgtcc cgcgtctgagg gtggcgatta 1200
aagttgttc 1210

<210> 127

<211> 282

<212> PRT

<213> Homo sapiens

<400> 127

Met	Ser	Gly	Gly	Trp	Met	Ala	Gln	Val	Gly	Ala	Trp	Arg	Thr	Gly	Ala
1					5						10				15

Leu	Gly	Leu	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Gly	Leu	Glu		
20											30			

Ala	Ala	Ala	Ser	Pro	Leu	Ser	Thr	Pro	Thr	Ser	Ala	Gln	Ala	Ala	Gly
35					40						45				

Pro	Ser	Ser	Gly	Ser	Cys	Pro	Pro	Thr	Lys	Phe	Gln	Cys	Arg	Thr	Ser
50						55					60				

Gly	Leu	Cys	Val	Pro	Leu	Thr	Trp	Arg	Cys	Asp	Arg	Asp	Leu	Asp	Cys
65					70				75				80		

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala
 225 230 235 240
 Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280
 <210> 128
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 128
 aagttccagt gccgcaccag tggc
 <210> 129

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 129
ttggttccac agccgagctc gtcg 24

<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 130
gaggaggaggt gcaaggattga gccatgtacc cagaaagggc aatgccacc 50
      50

<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1837)
<223> a, t, c or g

<400> 131
cccacgcgtc cggtctcgct cgctcgca gcggcgcaag cagaggtcgc gcacagatgc 60
gggttagact ggcgggggga ggaggcgagg gagggaaagg agctgcatgc atgagacc 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaacc 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcttg tggtttcagc tggcgctgtg ctccggccct gcacagctca 300
cgggcggtt cgtgatccctt caagtgtgtg ctgaccccg cattcccgag aatggcttca 360
ggaccccccag cgaggggtt ttctttaag gctctgtac ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tggatggaa gcattttaat ggaaccttag 480
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgcgtatc cctcaaatcg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaatac atcacttgtc 600
atgaaggatt caagatccgg taccggacc tacacaataat gtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gctcttcta 720
atggctatgt aaacatctt gagctccaga cctccccc ggtggggact gtatctcct 780
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accaaactgt gcccagcacc catgagaccc tcctgaccac gtggaaagatt gtggcgatc 1140

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cgccaaccag tgtgctgctg gtgctgctgc tcgtcatcct gccaggatg ttccagacca 1200
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 ctgatcctta aaattgctat gctgatagag tggtagggc tggaaagcttg atcaagtcct 1800
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1															15

5

10

15

Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
20														30

20

25

30

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
35															45

35

40

45

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
50															60

50

55

60

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
65															80

65

70

75

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
85															95

85

90

95

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
100															110

100

105

110

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
115															125

115

120

125

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
130															140

130

135

140

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
145															160

145

150

155

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
165															175

165

170

175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn,
 485 490

<210> 133
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133
 attcctatac gctgcttcc cg 23

<210> 134
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134
 agccaggatc gcagtaaaac tcc 23

<210> 135
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135
 atttaaac tt gatgggtctg cgtatcttga gtgcttacaa aaccttatct 50

<210> 136
 <211> 1815
 <212> DNA
 <213> Homo sapiens

<400> 136
 cccacgcgtc cgctccgcgc cctccccccc gcctcccggtg cgggtccgtcg gtggccctaga 60
 gatgctgctg ccgcgggtgc agttgtcgcg cacgcctctg cccgcgcagcc cgctccaccc 120
 ccgttagcgcc cgagtgtcg ggggcgaccc cgagtcgggc catgaggccg ggaaccgcgc 180
 tacaggccgt gctgctggcc gtgctgctgg tggggctgctg ggcgcgcacg ggtcgctgc 240
 ttagtgtcgc ggatttggac ctcagaggag ggcagccagt ctgcggggga gggacacacaga 300

ggccttgtta taaagtcat tacttccatg atacttcgt aagactgaac tttgaggaag 360
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcg catcgagtc gaagatgaac 420
 agaaaactgat agaaaagttc attgaaaacc tcttgcacat tgatggtagt ttctggattt 480
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
 ggactgtatgg cagcatatca caattttagga actggatgt ggatgagccg tcctgcggca 600
 gcgaggctcg cgtggcatg taccatcagc catcgccacc cgctggcatc ggaggcccct 660
 acatgttcca gtggatgtat gaccgggtca acatgaagaa caatttcatt tgcaaatatt 720
 ctgatgagaa accagcagtt ccttcttagag aagctgaagg tgaggaaaca gagctgacaa 780
 cacctgtact tccagaagaa acacaggaag aagatgcca aaaaacatt aaagaaaagta 840
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctccctcc 900
 ttgtggtcac cacagtgtt tggtgggtt ggatctgttag aaaaagaaaa cgggagcagc 960
 cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag gaaacagcc 1020
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactt gctgagaccc 1080
 ggcagacact gaagaatatt tcattccgag tgtgtcggg agaagccact cccgatgaca 1140
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 aaagatgggc tggagactt gaaaaaccac ctcttttc cttgtctat acagcagcac 1680
 atattatcat acagacagaa aatccagaat ctttcaaag cccacatatg gtacacagg 1740
 ttggcctgtg catcggaat tctcatatct gttttttca aagaataaaa tcaaataaaag 1800
 agcagaaaa aaaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
 1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
 20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
 35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
 50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
 85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
 100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 138
 gttcattgaa aacctttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 139
 aagccaaaga agcctgcagg aggg 24

<210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 140
 cagtccaagc ataaagggtcc tggc 24

<210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 141
 ggggtctccc tcagggccgg gaggcacage ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttccgcgg acttgggggc gcccgcgtgag ccccgccgc cgcagaagac 120
 ttgtgtttgc ctccgcaggc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180
 tggtgtgttc agcatgcgtc tgtggacccc agtggcggtc ctgacacctgc tggcgtaactg 240
 cctgcaccag cggcggtgg ccctggccga gctgcaggag gccgatggcc agtgtccgg 300
 cgaccgcagc ctgctgaagt taaaaatggt gcaggtcggt tttcgacacg gggctcgag 360
 tcctctcaag cccgtccgc tggaggagca ggttagagtgg aacccccacg tattagaggt 420
 cccaccccaa actcagttt attacacagt caccaatcta gctggtggtc cgaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctggca 540
 gctgaccaag gtgggcatgc agcaaatttttgc tgccttggga gagagactga ggaagaacta 600
 tgtgaaagac attcccttgc tttcaccaac cttcaacccca caggagggtct ttattcggtc 660
 cactaacatt tttcgaaatc tggagtccac ccgttggc tttccagtg 720

tcagaaaagaa ggaccatca tcatccacac tcatgaagca gattcagaag tcttgatcc 780
 caactaccaa agctgctgga gcctgaggca gagaaccaga gccggaggc agactgcctc 840
 ttacagcca ggaatctcg aggatttcaa aaaggtgaag gacaggatgg gcattgacag 900
 tagtgataaa gtggacttct tcatcctcct ggacaacgtg gtcggcggc aggacacaa 960
 cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
 cacatccttg tacatactgc ccaaggaaga cagggaaagt cttagatgg cagtaggccc 1080
 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
 gaccctgggg attttgacc acaaatggcc accgtttgc gttgaccta ccatgaaact 1260
 ttaccagcac ctggaatcta aggagtgggt tgcagctc tattaccacg ggaaggagca 1320
 ggtgccgaga ggttgcctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
 agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
 agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgattt aaaataaagt 1500
 gccttataac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met	Ile	Thr	Gly	Val	Phe	Ser	Met	Arg	Leu	Trp	Thr	Pro	Val	Gly	Val
1				5					10				15		

Leu	Thr	Ser	Leu	Ala	Tyr	Cys	Leu	His	Gln	Arg	Arg	Val	Ala	Leu	Ala
			20					25				30			

Glu	Leu	Gln	Glu	Ala	Asp	Gly	Gln	Cys	Pro	Val	Asp	Arg	Ser	Leu	Leu
			35				40				45				

Lys	Leu	Lys	Met	Val	Gln	Val	Val	Phe	Arg	His	Gly	Ala	Arg	Ser	Pro
			50				55			60					

Leu	Lys	Pro	Leu	Pro	Leu	Glu	Glu	Gln	Val	Glu	Trp	Asn	Pro	Gln	Leu
65					70				75			80			

Leu	Glu	Val	Pro	Pro	Gln	Thr	Gln	Phe	Asp	Tyr	Thr	Val	Thr	Asn	Leu
					85				90			95			

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu
					100				105			110			

Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly
						115			120			125			

Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val
						130		135			140				

Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe
						145			150		155		160		

Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu
						165			170			175			

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 235 240
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 315 320
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
 385 390 395 400
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
 405 410 415
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
 420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 143
 ccaactacca aagctgctgg agcc 24

<210> 144
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 144;
 gcagctctat taccacggga agga 24

<210> 145
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 145
 tccttcccggt ggtaatagag ctgc 24

<210> 146
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 146
 ggcagagaac cagaggccgg aggagactgc ctcttacag ccagg 45

<210> 147
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<400> 147
 ctccctttaa catacttgca gctaaaacta aatattgctg cttggggacc tcctttagc 60
 cttaaatttc agctcatcac cttcacctgc cttggtcatg gctctgctat tctccttgat 120
 ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180

gggcctccac	cgttgtgaag	ggcggttgg	ggtggAACAG	aaaggccagt	ggggcaccgt	240
gtgtgatgac	ggctggaca	ttaaggacgt	ggctgtgtg	tgccgggagc	tggctgtgg	300
agctgccagc	gaaaccccta	gtggtatttt	gtatgagcca	ccagcagaaa	aagagcaaaa	360
ggtcctcatc	caatcagtca	gttgcacagg	aacagaagat	acatggctc	agtgtgagca	420
agaagaagtt	tatgattgtt	cacatgatga	agatgctggg	gcatgtgtg	agaacccaga	480
gagctcttc	tccccagtcc	cagagggtgt	caggctggct	gacggccctg	ggcattgcaa	540
gggacgcgtg	gaagtgaagc	accagaacca	gtggataacc	gtgtccaga	caggctggag	600
cctccgggccc	gcaaagggtgg	tgtgcggca	gctggatgt	gggagggctg	tactgactca	660
aaaacgctgc	aacaaggcatg	cctatggccg	aaaacccatc	tggctgagcc	agatgtcatg	720
ctcaggacga	gaagcaaccc	ttcaggattt	cccttctggg	ccttggggga	agaacacctg	780
caaccatgtat	gaagacacgt	gggtcgaatg	tgaagatccc	tttacttga	gacttagtagg	840
aggagacaac	ctctgtctg	ggcgacttgg	ggtgtgcac	aaggcgtat	ggggctctgt	900
ctgtgatgac	aactggggag	aaaaggagga	ccaggtggta	tgcaagcaac	tggctgtgg	960
gaagtcctc	tctccctct	tcagagaccg	gaaatgctat	ggccctgggg	ttggccgcat	1020
ctggctggat	aatgttctgt	gctcagggg	ggagcagtcc	ctggagcagt	gccagcacag	1080
attttggggg	tttacgact	gcacccacca	ggaagatgtg	gctgtcatct	gctcagtgt	1140
ggtggccatc	atctaattctg	ttgagtgct	gaatagaaga	aaaacacaga	agaaggagc	1200
atttactgtc	tacatgactg	catggatga	acactgtatct	tcttctgccc	ttggacttgg	1260
acttataactt	ggtggccctg	attctcaggc	tttcagagg	ggatcagaac	ttacaacatc	1320
aggtctagtt	ctcaggccat	cagacatagt	tttggactac	atcaccacct	ttccatgtc	1380
tccacattgc	acacagcaga	ttcccagcct	ccataattgt	gtgtatcaac	tacttaata	1440
cattctcaca	cacacacaca	cacacacaca	cacacacaca	cacacataca	ccatttgc	1500
tgtttctctg	aagaactctg	acaaaataca	gattttggta	ctgaaaagaga	ttcttagagga	1560
acggaatttt	aaggataaat	tttctgaaatt	ggttatgggg	tttctgaaat	tggctctata	1620
atctaatttag	atataaaatt	ctggtaactt	tatttacaat	aataaagata	gcactatgt	1680
ttcaaa						1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met	Ala	Leu	Leu	Phe	Ser	Leu	Ile	Leu	Ala	Ile	Cys	Thr	Arg	Pro	Gly
1					5					10					15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
 50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
 100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu			
115	120	125	
Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro			
130	135	140	
Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr			
145	150	155	160
Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys			
165	170	175	
Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn			
180	185	190	
Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys			
195	200	205	
Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly			
210	215	220	
Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp			
225	230	235	240
Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg			
245	250	255	
Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn			
260	265	270	
Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly			
275	280	285	
Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly			
290	295	300	
Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln			
305	310	315	320
Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr			
325	330	335	
His Gln Glu Asp Val Ala Val Ile Cys Ser Val			
340	345		

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 149		
ttagctcat cacccatcacc tgcc		24
<210> 150		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 150		
ggctcataca aaataccact aggg		24
<210> 151		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 151		
gggcctccac cgctgtgaag ggcgggtgaa ggtggAACAG aaaggccagt		50
<210> 152		
<211> 1427		
<212> DNA		
<213> Homo sapiens		
<400> 152		
actgcactcg ttgttatccc cggggatccc ctagagatcc ctgcaccccg 60 accacacgcgt ccgcggacgc gtggggcgac gcgtggcccg gctaccagga agagtctgcc 120 gaaggtgtaaag gccatggact tcatcaccc cacagccatc ctgccccctgc tgttcggctg 180 cctggggcgtc ttccggctct tccggctgtc gcagtgggtg cgcggaaagg cctacctgcg 240 gaatgtgtgt gtggatca caggcgccac ctcaaggctg ggcaaaaat gtgcaaaaatg 300 cttctatgtct gcgggtgtta aactgggtct ctgtggccgg aatgggtgggg ccctagaaga 360 gctcatcaga gaacttaccg ctctcatgc caccaagggtg cagacacaca agccttactt 420 ggtgacccctc gacccacacg actctggggc catagttgca gcagcagctg agatctgc 480 gtgtttggc tatgtcgaca tacttgtcaa caatgtggg atcagctacc gtggtaccat 540 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600 tgctctaaccg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcg 660 catcagcagc atccaggcga agatgagcat tcctttcga tcagcatatg cagccctccaa 720 gcacgcaccc caggcttct ttgtactgtct gcgtggccgag atggAACAGt atgaaattga 780 ggtgaccgtc atcagccccg getacatcca caccaaccc tctgtaaaatg ccacccacccgc 840 ggatggatct aggtatggag ttatggacac cacccacagcc caggggccaa gccctgtgga 900 ggtgcccaag gatgttcttg ctgtgtggg gaagaagaag aaagatgtga tcctggctga 960 cttactgcct tccttggtc ttatcttcg aactctggct cctggccctct tcctcagcc 1020 catggcctcc agggccagaa aagagcggaa atccaaagaac tccttagtact ctgaccagcc 1080		

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
 ttgtttagac tttaatggag atttgtctca caagtggaa agactgaaga aacacatctc 1200
 gtgcagatct gctggcagag gacaatcaa aacgacaaca agcttctcc caggtgagg 1260
 ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
 tctcaaacag taaaaaaaaaaa aaaaaaggc ggcgcgact cttagactga cctgcagaag 1380
 ctggccgcc atggcccaac ttgttattt cagcttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met	Asp	Phe	Ile	Thr	Ser	Thr	Ala	Ile	Leu	Pro	Leu	Leu	Phe	Gly	Cys
							5							10	

Leu	Gly	Val	Phe	Gly	Leu	Phe	Arg	Leu	Leu	Gln	Trp	Val	Arg	Gly	Lys
								20				25			30

Ala	Tyr	Leu	Arg	Asn	Ala	Val	Val	Val	Ile	Thr	Gly	Ala	Thr	Ser	Gly
							35				40			45	

Leu	Gly	Lys	Glu	Cys	Ala	Lys	Val	Phe	Tyr	Ala	Ala	Gly	Ala	Lys	Leu
						50			55			60			

Val	Leu	Cys	Gly	Arg	Asn	Gly	Gly	Ala	Leu	Glu	Glu	Leu	Ile	Arg	Glu
							65		70		75		80		

Leu	Thr	Ala	Ser	His	Ala	Thr	Lys	Val	Gln	Thr	His	Lys	Pro	Tyr	Leu
							85		90			95			

Val	Thr	Phe	Asp	Leu	Thr	Asp	Ser	Gly	Ala	Ile	Val	Ala	Ala	Ala	Ala
						100		105			110				

Glu	Ile	Leu	Gln	Cys	Phe	Gly	Tyr	Val	Asp	Ile	Leu	Val	Asn	Asn	Ala
							115		120		125				

Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Ile	Met	Asp	Thr	Thr	Val	Asp	Val	Asp
								130		135		140			

Lys	Arg	Val	Met	Glu	Thr	Asn	Tyr	Phe	Gly	Pro	Val	Ala	Leu	Thr	Lys
						145		150		155		160			

Ala	Leu	Leu	Pro	Ser	Met	Ile	Lys	Arg	Arg	Gln	Gly	His	Ile	Val	Ala
						165		170			175				

Ile	Ser	Ser	Ile	Gln	Gly	Lys	Met	Ser	Ile	Pro	Phe	Arg	Ser	Ala	Tyr
							180		185			190			

Ala	Ala	Ser	Lys	His	Ala	Thr	Gln	Ala	Phe	Phe	Asp	Cys	Leu	Arg	Ala
							195		200		205				

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210

215

220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
 225 230 235 240

Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
 245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val
 260 265 270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
 275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu
 290 295 300

Arg Lys Ser Lys Asn Ser
 305 310

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154

ggtgctaaac tggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 156
 tcatactgtt ccatctcgac acgc 24

 <210> 157
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 157
 aatgggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

 <210> 158
 <211> 1771
 <212> DNA
 <213> Homo sapiens

 <400> 158
 cccacgcgtc cgctgggtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
 aaaaaaaaaaa acacaccaa cgcgtcgac cacaaaaagg atgaaatttc ttctggacat 120
 cctcctgctt ctccccgttac tgatcgctg ctcccttagag tccttcgtga agcttttat 180
 tcctaagagg agaaaaatcag tcacccggcga aatcgctg attacaggag ctggcatgg 240
 aattgggaga ctgactgcct atgaatttgc taaaacttaaa agcaagctgg ttctctggga 300
 tataaataag catggactgg agaaaaacagg tgccaaatgc aagggactgg gtgccaagg 360
 tcatacctt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaagg 420
 gaaggcagaa attggagatg ttagtatttt agtaaataat gctggtgtag tctatacatc 480
 agatttgttt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540
 acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
 tgtcactgtg gcttcggcag ctggacatgt ctgggtcccc ttcttactgg cttactgttc 660
 aagcaagtt gctgctgtt gatttcataa aacttgaca gatgaactgg ctgccttaca 720
 aataactgga gtc当地acaa catgtctgtg tcctaatttc gtaaacactg gtttcatcaa 780
 aaatccaagt acaagttgg gacccactct ggaacctgag gaagtggtaa acagctgt 840
 gcatgggatt ctgactgagc agaagatgat ttttattcca tcttctatag ctttttaac 900
 aacattggaa aggatcctc ctgagcgtt cctggcagtt taaaacgaa aaatcagtgt 960
 taagttttagt gcagttttagt gatataaaaat gaaagcgcaa taagcaccta gtttctgaa 1020
 aactgattta ccaggtttag gttgatgtca tctaatacgcc tccaaatgtt aatgtttgaa 1080
 ctctctttt ttcttaattt cccatttct tcaatatcat ttttgaggtt ttggcagtct 1140
 tcatttacta ccacttgttcc tttagccaaa agctgattac atatgatata aacagagaaa 1200
 tacctttaga ggtgacttta agaaaaatga agaaaaaagg cccaaatgac tttttaaaa 1260
 taatttccaa gattattgt ggctcacctg aaggcttgc aaaatttgc ccataaccgt 1320
 ttatattaaca tatatttttta tttagtattt cacttaattt ttgtataatt tttttttttt 1380
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 gccactctgt ttccctgagag atacctcaca ttccaatgcc aaacatttct gcacaggaa 1560
 gctagaggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattt 1620
 agagaatgta cccacaaatg gcagcaataa taaatggatc acactaaaaaaa aaaaaaaaaaa 1680
 aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 1740
 aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa a 1771

<210> 159

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
1			5				10						15	

Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
							20					30			

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
							35				40		45		

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
							50			55		60			

Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
							65		70		75		80		

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
							85			90		95			

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
							100			105		110			

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
							115			120		125			

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
							130		135		140				

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
							145		150		155		160		

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
							165			170		175			

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
							180			185		190			

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
							195		200		205				

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
							210		215		220				

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
							225		230		235		240		

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
							245			250		255			

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 161

atccccatgca tcagcctgtt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 162

gctgggttag tctatacacatc agattttttt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgccggacgcg tgggtcgact agttctagat cgcgagcgcc cgcccgccgc 60
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaaagg 120

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
1 5 . 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
20 25 30

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln			
85		90	95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100		105	110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115		120	125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130		135	140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145		150	155
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165		170	175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180		185	190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195		200	205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210		215	220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225		230	235
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245		250	255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260		265	270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275		280	285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290		295	300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305		310	315
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325		330	335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340		345	350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 165

ttccatgccca cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 167
 agctctcaga ggctggtcat aggg 24

<210> 168
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 168
 gtcggccctt tcccaggact gaacatgaag agttatgcgg gcttcctcac 50

<210> 169
 <211> 2477
 <212> DNA
 <213> Homo sapiens

<400> 169
 cgagggcttt tccggctccg gaatggcaca tgtggaaatc ccagtcttgt tggctacaac 60
 atttttccct ttccctaacaa gttctaacag ctgttctaac agcttagtgat caggggttct 120
 tcggctggaa gaagaaaggg ctgaggcgac agcaggcac tctcaactcgag ggtgaccagc 180
 tcctgcctc tctgtggata acagagcatg agaaaatgaa gagatgcgcg ggagtggat 240
 gatgaaatgc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300
 cctggagagc ctgggggagg gcctgcctaa caagcttca aaaaacagga gcgacttcca 360
 ctgggctggg ataagacgtc ccgtaggat agggaaagact gggttagtc ctaatataa 420
 attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacatgg 480
 cttaaggggc cagaaataga gatgcttgc taaaataat ttaaaaaaaaa gcaagtattt 540
 tatagcataa aggctagaga caaaaataga taacaggatt ccctgaacat tcctaagagg 600
 gagaaatgt gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
 accaggatgg ggaccctggg tcaggccagc ctcttgctc ctccccggaaa ttattttgg 720
 tctgaccact ctgccttggt tttgcagaa tcatgtgagg gccaaccggg gaaggtggag 780
 cagatgagca cacacaggag ccgtctcctc accggcccc ctctcagcat ggaacagagg 840
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 ctcatcaaga tcccttcaga caccctggcc ctggctccc actttgacat cttctacatc 1560
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 aggggttaat tttgtgactt agttcttagc tacttcctcc agccatcagt cattgggtat 2400
 gtaaggaatg caagcgatttcaatatttc ccaaacttta agaaaaaaact ttaagaaggt 2460
 acatctgcaaa aagcaaa 2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met	Gly	Thr	Leu	Gly	Gln	Ala	Ser	Leu	Phe	Ala	Pro	Pro	Gly	Asn	Tyr
1															

5

10

15

Phe	Trp	Ser	Asp	His	Ser	Ala	Leu	Cys	Phe	Ala	Glu	Ser	Cys	Glu	Gly
20															

25

30

Gln	Pro	Gly	Lys	Val	Glu	Gln	Met	Ser	Thr	His	Arg	Ser	Arg	Leu	Leu
35															

40

45

Thr	Ala	Ala	Pro	Leu	Ser	Met	Glu	Gln	Arg	Gln	Pro	Trp	Pro	Arg	Ala
50															

55

60

Leu	Gl	U	Val	Asp	Ser	Arg	Ser	Val	Val	Leu	Leu	Ser	Val	Val	Trp	Val
65																

65

70

75

80

Leu	Leu	Ala	Pro	Pro	Ala	Ala	Gly	Met	Pro	Gln	Phe	Ser	Thr	Phe	His
85															

85

90

95

Ser	Glu	Asn	Arg	Asp	Trp	Thr	Phe	Asn	His	Leu	Thr	Val	His	Gln	Gly
100															

100

105

110

Thr	Gly	Ala	Val	Tyr	Val	Gly	Ala	Ile	Asn	Arg	Val	Tyr	Lys	Leu	Thr
115															

115

120

125

Gly	Asn	Leu	Thr	Ile	Gln	Val	Ala	His	Lys	Thr	Gly	Pro	Glu	Glu	Asp
130															

130

135

140

Asn	Lys	Ser	Arg	Tyr	Pro	Pro	Leu	Ile	Val	Gln	Pro	Cys	Ser	Glu	Val
145															

145

150

155

160

Leu	Thr	Leu	Thr	Asn	Asn	Val	Asn	Lys	Leu	Leu	Ile	Ile	Asp	Tyr	Ser
165															

165

170

175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
 260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
 275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

100

450

455

460

Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
465 470 475 480

Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
485 490 495

Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
500 505 510

Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
515 520 525

Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
530 535 540

Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171

tggaaataccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172

ctttgcctt ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173
 ggactcactg gcccaggcct tcaatatcac cagccaggac gat 42

 <210> 174
 <211> 3106
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (1683)
 <223> a, t, c or g

 <400> 174
 aggctcccgc gcggggctga gtgcggactg gagtggaaac ccgggtcccc gcgcttagag 60
 aacacgcgt gaccacgtgg agcctccggc ggaggccgc cccacgcgt ggactccgtc 120
 tgctggctgt ctggggcttc ctgggtgtcc gcaggctgga ctggagcacc ctggttccctc 180
 tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctggacttc atgctggagg 240
 attccacctt ctggatcttc gggggctcca tccactattt ccgtgtgcc agggagta 300
 ggagggaccg cctgctgaag atgaaggcct gtggctgaa caccctcacc acctatgttc 360
 cgtgaacct gcatgagcca gaaagaggca aatttgactt ctctggaaac ctggacctgg 420
 aggcccttgt cctgatggcc gcaagatcg ggctgtgggt gattctgcgt ccaggcccct 480
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 aggctgtcg gctgtctcta gggggggagc agctaattcag atcgcccagc ctttgcct 2280

cagaaaaaagt	gctgaaacgt	gcccttcac	cgacgtcac	agccctgcga	gcacatctgtc	2340
gactcaggcg	tgtctttgc	tggttctgg	gaggcgttgc	cacatccctc	atggccccat	2400
tttatccccg	aatcctggg	tgtgtcacca	gttagaggg	tgggaaaggg	gtgtctcacc	2460
ttagctgact	ttgttcttc	ttcacaaacct	tctgagccctt	ctttgggatt	ctggaaaggaa	2520
ctcggcgtga	gaaacatgtg	acttcccctt	tcccttccta	ctcgctgctt	cccacagggt	2580
gacaggctgg	gctggagaaa	cagaaatcct	caccctgcgt	cttcccaagt	tagcaggtgt	2640
ctctgggttt	cagtggggag	gacatgtgag	tcctggcaga	agccatggcc	catgtctgca	2700
catccaggga	ggaggacaga	aggcccagct	cacatgtgag	tcctggcaga	agccatggcc	2760
catgtctgca	catccaggga	ggaggacaga	aggcccagct	cacatgtgag	tcctggcaga	2820
agccatggcc	catgtctgca	catccaggga	ggaggacaga	aggcccagct	cacatgtgag	2880
tcctggcaga	agccatggcc	catgtctgca	catccaggga	ggaggacaga	aggcccagct	2940
cagtggcccc	cgtccccac	cccccaacgcc	cgaacagcag	ggcagagca	gccttccttc	3000
gaagtgtgtc	caagtccgca	tttgagcctt	gttctggggc	ccagccaaac	acctggcttg	3060
ggctcaactgt	cctgagttgc	agtaaaagcta	taaccttcaa	tcacaa		3106

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD RES

<222> (539)

<223> Any amino acid

<400> 175

Met	Thr	Thr	Trp	Ser	Leu	Arg	Arg	Arg	Pro	Ala	Arg	Thr	Leu	Gly	Leu
1				5					10				15		

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
 35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
 65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160

Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175

His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190

Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205

Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220

Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240

Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255

Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270

Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285

Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300

Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320

Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335

Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350

Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365

Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380

Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400

Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415

Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60
 ccctggtag ggttctctac ttggcattcg gtgggggtca agacgcaggc acctacgcca 120
 aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttgg 180
 ggaatccgac acgtgacggt ctgtccgccc tctcagacta gaggagcgct gtaaacgcca 240
 tggctcccaa gaagctgtcc tgccctcggt ccctgctgct gccgctcagc ctgacgctac 300
 tgctccccca ggcagacact cggtcggtcg tagtgatag gggtcatgac cggttctcc 360
 tagacggggc cccgttcgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

tgcttggc cgaccggc ttgaagatgc gatggagcgg cctcaacgcc atacagttt 480
 atgtgccctg gaactaccac gagccacagc ctgggtcta taacttaat ggcagccgg 540
 acctcattgc ctttctgaat gaggcagctc tagcAACCT gtgggtcata ctgagaccag 600
 gacccatct ctgtcagag tggagatgg ggggtctccc atccctggttt ctccggaaac 660
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcaatggac tcctgggtca 720
 aggtcttgct gccccagata tatccatggc tttatcacaa tggggcaac atcattagca 780
 ttcaggtgga gaatgaatat gtagctaca gagcctgtga cttcagctac atgaggcact 840
 tggctggct cttccgtca ctgttaggag aaaagatctt gctcttacc acagatggc 900
 ctgaaggact caagtgtggc tccctccggg gacttatac cactgttagat ttggccag 960
 ctgacaacat gaccaaaatc tttaccctgc ttccggaa tgaaccccat gggcattgg 1020
 taaactctga gtactacaca ggctggctgg attactggg ccagaatcac tccacacgg 1080
 ctgtgtcagc tgtaacccaa ggactagaga acatgtcaa gttgggagcc agtgtgaaca 1140
 tgtacatgtt ccatggaggt accaactttg gatattggaa tgggtccgat aagaaggac 1200
 gtttccttcc gattactacc agctatgact atgatgcacc tatatctgaa gcaggggacc 1260
 ccacacctaa gcttttgc cttcgagatg tcacagcaa gttccaggaa gttccttgg 1320
 gaccttacc tccccggc cccaaatgtga tgcttggacc tggactctg cacctgggt 1380
 ggcatttact ggcttccta gacttgcctt gccccgtgg gccattcat tcaatctgc 1440
 caatgaccc ttgggtctgc aaggaggacc atggctcat gttgtaccga accttatg 1500
 cccataccat ttttggcca acaccattct ggggcacaa taatggagtc catgaccgt 1560
 cctatgtat ggtggatggg gtgtccagg gtgtgtgga gcaaatatg agagacaaac 1620
 tattttgac ggggaaactg gggccaaac tggatatctt ggtggagac atggggaggc 1680
 tcagcttgg gtctaacagc agtacttca agggcctgtt gaagccacca attctgggc 1740
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 ggttccctt ccagttggc aaatggccat atcctcaagc tccttctgg cccacattct 1860
 actccaaac atttccaaatt ttaggctca gttgggacac atttctatat ctacctggat 1920
 ggaccaaggg ccaagtcgg atcaatgggt ttaacttggg ccgtactgg acaaagcagg 1980
 ggcacacaaca gaccctctac gtggcaagat tcctgctgtt tccttagggg gccctcaaca 2040
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 agcctatcct caatagcaact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
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 ggtggctcat gcctgtatc ccagcactt gggaggctga gacgggtgga ttacctgagg 2280
 tcaggactc aagaccagcc tggcaacat ggtgaaaccc cgtctccact aaaaatacaa 2340
 aaattagccg ggcgtatgg tggcacctc taatcccacg tacttggag gctgagggca 2400
 ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggaggttgc accactgcac 2460
 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu

1

5

10

15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val

20

25

30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr

35

40

45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala

50

55

60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
 85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
 100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
 115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
 130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
 145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
 165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
 180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
 195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
 210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Val Asp Phe Gly Pro
 225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
 245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
 260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
 275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
 290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
 305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
 325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 179

tggacaaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 180

gggcattcacc gaaggcgtgg acctttatgg tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 181

ccagctatga ctatgtatca cc

22

<210> 182
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182
 tggcacccag aatggtgtt gctc 24

<210> 183
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac cttaacctcc 50

<210> 184
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<400> 184
 gcttgaaca cgtctgcagg cccaaagtgg agcatctgat tggttatggat gtatttgagt 60
 gcaccaccaa tatggcttac atggaaaaa agcttctcat cagttacata tccattattt 120
 gtgttatgg ctatctgc ctctacactc tcttctgggtt attcaggata cctttaagg 180
 aatattctt cggaaaatgc agagaagaga gcagtttag tgacattcca gatgtaaaa 240
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaaaggcg 300
 ttgggtgttt cttgtcagaa gtttagtggaaa ataaaacttag gggaaatttagt ttgaaccatg 360
 agtggacatt tgaaaaactc aggccgcaca ttccacgca cggccaggac aagcaggagt 420
 tgcacatgtt catgctgtcg ggggtgcgg atgctgtctt tgacctcaca gacctggatg 480
 tgctaaagct tgaactaatt ccagaagcta aaattctgc taagattctt caaatgacta 540
 accttcaaga gctccaccc tgccactgccc ctgcaaaatg tgaacagact gcttttagct 600
 ttcttcgcga tcacttgaga tgccctcagc tgaagttcac tggatgtggct gaaattcctg 660
 cctgggtgtta ttgtctaaa aaccttgcgg agttgtactt aataggcaat ttgaactctg 720
 aaaacaataa gatgatagga cttgaatctc tccgagatggt ggggcacccctt aagattctcc 780
 acgtgaagag caatttgacc aaagttccctt ccaacattac agatgtggct ccacatctt 840
 caaagtttagt cattcataat gacggcacta aactcttggt actgaacacgc cttaagaaaa 900
 tggatgtatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
 ttttcagccct ctctaattt cagaactggg atttaaagtgc caataacattt cggcacaattt 1020
 agggaaatcat cagtttccag cattaaaaac gactgacttg tttaaaaattt tggcataaca 1080
 aaattgttac tattcctccc tcttattaccc atgtaaaaa ctgggatgtca cttaatttctt 1140
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag ttacagaaaa ctcagatgtct 1200
 tagatgtgag ctacaacaaat tttcaataga aataggattt gttcagaacc 1260
 tgcagcattt gcatatcact gggaaacaaag tggacattctt gccaaaacaa ttgtttaat 1320

gcataaaagtt	gaggactttt	aatctggac	agaactgcat	cacccactc	ccagagaaaag	1380
tttgtcagct	ctccccagctc	actcaagtgg	agctgaaggg	gaactgcttg	gaccgcctgc	1440
cagcccagct	ggcccgagtgt	cggatgctca	agaaaaagcgg	gcttgggttg	gaagatcacc	1500
tttttgatac	cctgccactc	gaagtc当地	aggcattgaa	tcaagacata	aatattccct	1560
ttgcaaatgg	gatttaaact	aagataatat	atgcacagtg	atgtgc当地	acaaacttcct	1620
agattgcaag	tgctcacgta	caagtttata	caagataatg	catttttagga	gtagatacat	1680
cttttaaaat	aaaacagaga	ggatgcatag	aaggctgata	gaagacataa	ctgaatgttc	1740
aatgtttgtt	gggttttaag	tcatttcattt	ccaaatcatt	tttttttttc	ttttggggaa	1800
agggaaaggaa	aaattataat	cactaatctt	ggttctttt	aaattgtttg	taacttggat	1860
gctccgctta	ctgaatgttt	acaaattgct	tgcctgctaa	agtaaatgat	taaattgaca	1920
ttttcttact	aaaaaaaaaa	aaaaaaaa				1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
1 5 10 15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
20 25 30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
35 40 45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
50 55 60

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
65					70					75					80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
85 90 95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
 100 105 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
115 120 125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
130 135 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
145 150 155 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
 180 185 190

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465 470 475 480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro
485 490 495

Phe Ala Asn Gly Ile
500

<210> 186
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 186
cctccctcta ttacccatgt c 21

<210> 187
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 187
gaccaacttt ctctgggagt gagg 24

<210> 188
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 188
gtcactttat ttctctaaca acaagctcgatccttacca gtggcag 47

<210> 189
<211> 2917
<212> DNA
<213> Homo sapiens

<400> 189
ccccacgcgtc cggccttctc tctggacttt gcatttccat tcctttcat tgacaaaactg 60
actttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgcctctggg 120
aaacatcttq tgttttacac acataaggat ctgtgtttgg ggttttcttcttccctgg 180

gcattggcat	tgccttagtgg	ttgtgtgggg	agggagacca	cgtgggctca	gtgcttgc	240
gcacttatct	gcctaggta	atcgaagtct	tttgacccctc	atacagtgt	tatgcctg	300
atcgctgg	gtatcctggc	ggcctgctc	ctgctgatag	ttgtcg	ctgtcttac	360
ttcaaaatac	acaacgcgc	aaaagctgca	aaggaaccc	aagctgtgg	tgtaaaaat	420
cacaacc	cagaagg	gtggccaag	aacagccagg	ccaaaaccat	tgccacggag	480
tctgtcctg	ccctgcag	ctgtgaagga	tatagaatgt	gtgccag	tgattccctg	540
ccaccttgct	gttgcgacat	aatgagg	ctctgagta	ggaaagg	ccttc	600
gcagagccct	gaagactca	atgatgt	tgaggccacc	tg	gtcaggcac	660
agaagaaagg	cacagctccc	catca	atggaaaata	actc	tgctggaa	720
cagctgtgg	agatccctac	agagaget	cactggggc	aacc	ggaaggag	780
qqggagagag	aaccctca	gtgggaat	ctgataaa	agt	ctgctctatt	840
ctcacacaaa	tctacccctt	g	actgac	tc	tgtccagaaa	900
gctgatgt	taa	ca	atgg	cc	gcgccttg	960
aaaatgg	gagc	at	gg	ctt	ctgttgg	1020
gagctgaca	aa	tg	gg	cc	aggggg	1080
aatatggcag	agacccacaa	agccatgat	ctgcaact	atcc	gaactgc	1140
tggacaatag	aaagacc	aaacaaa	atcagaat	tctt	tgtccag	1200
gatccagatg	gaagctgt	aagt	aaaac	attaa	ctccag	1260
gggcctctgc	tagg	ctg	actat	gtt	tgaat	1320
tccagtacat	tgac	at	at	ttc	catca	1380
gtcttctact	actt	ttct	tc	ctt	aactgt	1440
accttgg	gat	c	ccca	cc	gtcg	1500
tgtgtgt	gc	acata	aa	act	aa	1560
ttccttag	aaa	tagacaa	at	ttt	gg	1620
accaactctg	gc	ctgatt	ac	ttt	ccat	1680
tcaaactctc	tgact	gtcg	tt	ccat	ttat	1740
gcttc	taca	tt	ca	cc	gtt	1800
gacaggatg	gat	ttt	at	cc	ttt	1860
aacttgc	aa	ttt	ca	cc	ttt	1920
gtccctt	at	ttt	ca	cc	ttt	1980
aatataatca	cc	ttt	ca	cc	ttt	2040
cagattatt	tga	at	ttt	ca	cc	2100
gaagatgat	taata	at	ttt	ca	cc	2160
tttgaatcca	att	ttt	ca	cc	ttt	2220
caaactctt	tt	ttt	ca	cc	ttt	2280
gatacctgta	gag	ctt	ca	cc	ttt	2340
agtggatgta	gtc	gag	tt	ca	cc	2400
ttccagtt	at	gc	tt	ca	cc	2460
gttttgat	at	gc	tt	ca	cc	2520
agcaaac	ac	ttt	ca	cc	ttt	2580
ctgaaaagg	at	cg	at	cc	ttt	2640
gaaactcc	ac	ca	ct	cc	ttt	2700
aatgttgt	ct	tg	at	cc	ttt	2760
aaatacc	ag	tc	ca	cc	ttt	2820
tccaggatg	ca	aa	cc	cc	ttt	2880
ggcctgaa	tg	ac	ca	cc	ttt	2917

<210> 190
<211> 607
<212> PRT
<213> *Homo sapiens*

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
 1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
 20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
 260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
 290 295 300
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
 305 310 315 320
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
 325 330 335
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
 340 345 350
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
 355 360 365
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
 370 375 380
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
 385 390 395 400
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
 405 410 415
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
 420 425 430
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
 435 440 445
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
 450 455 460
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
 465 470 475 480
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
 485 490 495
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
 500 505 510
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
 515 520 525
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
 530 535 540
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
 545 550 555 560
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565

570

575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe
 580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr
 595 600 605

<210> 191

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 191

tctctattcc aaactgtggc g

21

<210> 192

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 192

tttgatgacg attcgaaggt gg

22

<210> 193

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc

47

<210> 194

<211> 2362

<212> DNA

<213> Homo sapiens

<400> 194

gacggaagaa cagcgctccc gagggccgcgg gagcctgcag agaggacagc cggcctgcgc 60
 cgggacatgc ggccccagga gctccccagg ctgcgcgttcc cgttgcgtgc gttgcgttg 120
 ctgcgtgc cggccgcgc gtgcctgcc cacagcgcca cgcgcgttcga cccccacctgg 180

gagtccctgg acgcccccca gctgcccgcg tggttgacc aggccaagtt cggcatcttc 240
 atccactggg gagtgtttc cgtcccagc ttccggtagcg agtggttctg gtggtattgg 300
 caaaaaggaaa agataccgaa gatatgtggaa tttatgaaag ataattacc cccatgtttc 360
 aaatatgaag attttggacc actatttaca gcaaaaattt ttaatgccaa ccagtggca 420
 gatattttc aggccctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
 tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccag 540
 agggacattg tcaaggaaact tgaggttagcc attaggaaca gaactgaccc gcttttgg 600
 ctgtactatt cccttttga atggttcat ccgctcttc ttgaggatga atccagttca 660
 ttcataaagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgAAC 720
 aactatcagc ctgaggttct gtggcggat ggtgacggag gggcaccggc tcaatactgg 780
 aacagcacag gcttcttgc ctggttat aatgaaagcc cagttcgggg cacagtagtc 840
 accaatgatc gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900
 gatcgttata acccaggaca tctttgcca cataaaatggg aaaactgcat gacaatagac 960
 aaactgtcct ggggctatag gagggaaagct ggaatctctg actatcttac aattgaagaa 1020
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 cccacactag atggcaccat ttctgttagt tttgaggagc gactgaggca agtggggtcc 1140
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 cattgatttgc tttccatgtg tgactcagag gtgagaattt ttccacat tagtagcaag 1740
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 tatatagtta tgcacactt aatatggggat tttttctgg gaatgcatt gctgtcaat 1860
 tttttttgtt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920
 cacacctaattt gtgtatggta tagactgttgc tcccttaggct acagacatat acagcatgtt 1980
 actgaataact gtaggcataa gtaacagtgg tatttgcata tcgaaacata tggaaacata 2040
 gagaaggtac agtaaaaata ctgtaaaata aatgggtcact ctgtataggg cacttaccac 2100
 gaatggagct tacaggactg gaagttgctc tgggtgagtc agtgagtgaa tgtgaaggcc 2160
 taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220
 ttataaaaaaa aagttttctt ttcttcaatt ataaattaac ataaatgtac tggtaacttta 2280
 caaacgtttt aatttttaaa accttttgg ctctttgttataacactta gcttaaaaaca 2340
 taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met	Arg	Pro	Gln	Glu	Leu	Pro	Arg	Leu	Ala	Phe	Pro	Leu	Leu	Leu
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Leu	Leu	Leu	Leu	Pro	Pro	Pro	Cys	Pro	Ala	His	Ser	Ala	Thr	
20														30

Arg	Phe	Asp	Pro	Thr	Trp	Glu	Ser	Leu	Asp	Ala	Arg	Gln	Leu	Pro	Ala
35														45	

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
 50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
 100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
 115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
 130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
 145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
 165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
 180 185 190

Glu Asp Glu Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
 195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Ala Pro Asp Gln Tyr Trp Asn Ser
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460

Asn Val Ile
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 196

tggtttgacc aggccaaagt t cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 197

ggatttcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 198
 aacttgcagc atcagccact ctgc 24

<210> 199
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 199
 ttccgtgccc agcttcggta gcgagtggtt ctgggttgtat tggca 45

<210> 200
 <211> 2372
 <212> DNA
 <213> Homo sapiens

<400> 200
 agcaggaaaa tccggatgtc tcggttatga agtggagcag tgagtgttag cctcaacata 60
 gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120
 catctgaggt gttccctgg ctctgaaggg gtggcacga tggccaggtt cttagcgcctg 180
 gtgttgcctc tcacttccat ctggaccacg aggctcctgg tccaaggctc ttgcgtgca 240
 gaagagctt ccattccagggt gtcatgcaga attatgggta tcacccttgtt gagcaaaaag 300
 gcgaaccacgc agctgaattt cacagaagct aaggaggcct gtaggctgtt gggactaagt 360
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
 ggctgggttg gagatggatt cgtggtcato tctaggatta gcccaaacc caagtgtggg 480
 aaaaatgggg tgggtgcctt gatttggaaat gttccagtga gccgacagtt tgcagcctat 540
 ttttacaact catctgatac ttggactaacat tcgtgcattc cagaaaattat caccacaaaa 600
 gatccccat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgacagt 660
 acctactcggttgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agttttatg 780
 gaaactagca ccatgtctac agaaactgaa ccatttttttgg aaaataaaagc agcatcaag 840
 aatgaagctg ctgggtttgg aggtgtcccc acggctctgc tagtgcttgc tctcccttcc 900
 tttgtgtctg cagctggctt tggattttgc tatgtcaaaa ggtatgtgaa ggccttccct 960
 ttttacaaaca agaatcagca gaaggaaatg atcgaacca aagttagtaaa ggaggagaag 1020
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 aagagtccaa gcaaaaactac cgtgcgtgc ctggaaagctg aagtttagat gagacagaaaa 1140
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 cactgtttag aacacacaca cttactttt ctggctctca ccactgctga tattttctct 1860
 aggaaatata ctttacaag taacaaaaat aaaaactctt ataaatttct attttatct 1920
 gagttacaga aatgattact aagaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
 ttcaacaaac atttgcgaa tagtactat atgtcaagt ctgtgcaagg tattacactc 2040
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 tttttcagt tttgatattt ctagcttac tacttccaaa ctaatttttta ttttgctga 2160
 gactaatctt attcatttc tctaataatgg caaccattat aaccttaatt tattattaac 2220
 atacctaaga agtacattgt tacctctata taccaaagca cattttaaaaa gtgccattaa 2280
 caaatgtatc actagccctc cttttccaa caagaaggaa ctgagagatg cagaatattt 2340
 tgtgacaaaaa aattaaagca tttagaaaaac tt 2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr
1															15

Thr	Arg	Leu	Leu	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile
															30
20								25							

Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala
35						40						45			

Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu
50					55				60						

Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala
65					70				75			80			

Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val
85								90				95			

Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly
100						105						110			

Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys
115					120							125			

Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile
130					135					140					

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175

Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Val Pro Thr Ala Leu
 225 230 235 240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255

Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285

Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300

Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320

Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202

gagcttcca tccagggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 203
 gtcagtgaca gtacctactc gg

22

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 204
 tggaggcagga ggagtagtag tagg

24

<210> 205
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 205
 aggaggccctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206
 <211> 1620
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (973)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (977)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (996)
 <223> a, t, c or g

<220>
 <221> modified_base

<222> (1003)

<223> a, t, c or g

<400> 206

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 gaaaaactgcc gccgctctgc cacggctctgc ccacccaaacg cgaagacggg aaccctgtg 180
 actttgactg gagagaagtg gagatcctga tgtttcttag tgccattgtg atgatgaaga 240
 acccgagatc catcaactgtg gagacaacata taggcaacat tttcatgttt agtaaagtgg 300
 ccaacacaat tctttcttc cgcttggata ttgcgcattgg cctactttac atcacactct 360
 gcatagtgtt cctgatgacg tgcaaaccctt ccctatatat gggccctgag tatataaagt 420
 acttcaatga taaaaccatt gatgaggaac tagaacggga caagagggtc acttgattg 480
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 tctcccttaa atacaactgt acagggctaa attttggaa ggtggatgtt ggacgctata 600
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 tgatcctgtt ccaagggtgc aaggaggcaa tgccggcc acagattgac aagaaaggac 720
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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met	Ala	Val	Leu	Ala	Pro	Leu	Ile	Ala	Leu	Val	Tyr	Ser	Val	Pro	Arg
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5

10

15

Leu	Ser	Arg	Trp	Leu	Ala	Gln	Pro	Tyr	Tyr	Leu	Leu	Ser	Ala	Leu	Leu

20

25

30

Ser	Ala	Ala	Phe	Leu	Leu	Val	Arg	Lys	Leu	Pro	Pro	Leu	Cys	His	Gly

35

40

45

Leu	Pro	Thr	Gln	Arg	Glu	Asp	Gly	Asn	Pro	Cys	Asp	Phe	Asp	Trp	Arg

50

55

60

Glu	Val	Glu	Ile	Leu	Met	Phe	Leu	Ser	Ala	Ile	Val	Met	Met	Lys	Asn

65

70

75

80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
 145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
 165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
 195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
 225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
 245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
 260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
 275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys
 290 295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 208

gcttggatat tcgcatggc ctac

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 209
 tggagacaat atccctgagg 20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 210
 aacagttggc cacagcatgg cagg 24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 211
 ccattgtatga ggaactagaa cgggacaaga gggtcaacttg gattgtggag 50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met	Gly	Leu	Leu	Leu	Leu	Val	Pro	Leu	Leu	Leu	Leu	Pro	Gly	Ser	Tyr
1															

Gly	Leu	Pro	Phe	Tyr	Asn	Gly	Phe	Tyr	Tyr	Ser	Asn	Ser	Ala	Asn	Asp
					20			25							30

Gln	Asn	Leu	Gly	Asn	Gly	His	Gly	Lys	Asp	Leu	Leu	Asn	Gly	Val	Lys
					35			40							45

Leu	Val	Val	Glu	Thr	Pro	Glu	Glu	Thr	Leu	Phe	Thr	Tyr	Gln	Gly	Ala
					50			55							60

Ser	Val	Ile	Leu	Pro	Cys	Arg	Tyr	Arg	Tyr	Glu	Pro	Ala	Leu	Val	Ser
					65			70							80

Pro	Arg	Arg	Val	Arg	Val	Lys	Trp	Trp	Lys	Leu	Ser	Glu	Asn	Gly	Ala
					85			90							95

Pro	Glu	Lys	Asp	Val	Leu	Val	Ala	Ile	Gly	Leu	Arg	His	Arg	Ser	Phe
					100			105							110

Gly	Asp	Tyr	Gln	Gly	Arg	Val	His	Leu	Arg	Gln	Asp	Lys	Glu	His	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125	
Val Ser Leu Glu Ile Gln Asp	Leu Arg Leu Glu Asp	Tyr Gly Arg Tyr	
130	135	140	
Arg Cys Glu Val Ile Asp Gly	Leu Glu Asp Glu Ser Gly	Leu Val Glu	
145	150	155	160
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg			
165	170		175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala			
180	185		190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly			
195	200	205	
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr			
210	215	220	
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro			
225	230	235	240
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp			
245	250		255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu			
260	265	270	
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu			
275	280	285	
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys			
290	295	300	
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser			
305	310	315	320
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu			
325	330		335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr			
340	345	350	
Gly Val Tyr Cys Tyr Arg Gln His			
355	360		

<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215

ttcccttgtg ggttggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217

agccagttag gaaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218

tgtccaaagt acacacacacct gagg

24

<210> 219
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 219
 gatgccacga tcgccaagg tggacagctc tttgcgcctt ggaag 45

<210> 220
 <211> 1503
 <212> DNA
 <213> Homo sapiens

<400> 220
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 tggccagggg agggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgccc 180
 cggaaacttc cagtagcacc atgaggctt cctggacgg gaagtggcca aggaattcga 240
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 cgacggcgt gtgggttggg aggagctgca caacgcacc tatggccact acgcgccccgg 480
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 ggagggactg gacagaaaca aagatggcta tgtccaggtg gaggagtaca tcgcggatct 720
 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcgtt 780
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 ggtgctgccc cctgcccagg accagccctt ggtggaagcc aaccacctgc tgcacgagag 900
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 tgccctggct ggcctggac acctcctctc tgccaggagg caataaaaagc cagccccggg 1440
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaa 1503

<210> 221
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 221
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

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Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly			
20	25	30	
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala			
35	40	45	
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val			
50	55	60	
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu			
65	70	75	80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp			
85	90	95	
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg			
100	105	110	
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp			
115	120	125	
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly			
130	135	140	
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr			
145	150	155	160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp			
165	170	175	
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu			
180	185	190	
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr			
195	200	205	
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu			
210	215	220	
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Pro Ala			
225	230	235	240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn			
245	250	255	
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro			
260	265	270	
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu			
275	280	285	

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 225
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt 44
 <210> 226
 <211> 2403
 <212> DNA
 <213> Homo sapiens
 <400> 226
 gggcccttgc cttecgcaact cgggcgcagc cgggtggatc tcgagcagggt gcggagcccc 60
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 aaa 2403

<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

Met	Ser	Ala	Ala	Trp	Ile	Pro	Ala	Leu	Gly	Leu	Gly	Val	Cys	Leu	Leu
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Leu	Leu	Pro	Gly	Pro	Ala	Gly	Ser	Glu	Gly	Ala	Ala	Pro	Ile	Ala	Ile
							20		25				30		

Thr	Cys	Phe	Thr	Arg	Gly	Leu	Asp	Ile	Arg	Lys	Glu	Lys	Ala	Asp	Val
							35		40			45			

Leu	Cys	Pro	Gly	Gly	Cys	Pro	Leu	Glu	Glu	Phe	Ser	Val	Tyr	Gly	Asn
							50		55			60			

Ile	Val	Tyr	Ala	Ser	Val	Ser	Ser	Ile	Cys	Gly	Ala	Ala	Val	His	Arg
								65	70		75		80		

Gly	Val	Ile	Ser	Asn	Ser	Gly	Gly	Pro	Val	Arg	Val	Tyr	Ser	Leu	Pro
							85		90			95			

Gly	Arg	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ala	Asn	Gly	Ile	Gln	Ser	Gln
							100		105			110			

Met	Leu	Ser	Arg	Trp	Ser	Ala	Ser	Phe	Thr	Val	Thr	Lys	Gly	Lys	Ser
							115		120			125			

Ser	Thr	Gln	Glu	Ala	Thr	Gly	Gln	Ala	Val	Ser	Thr	Ala	His	Pro	Pro
							130		135			140			

Thr	Gly	Lys	Arg	Leu	Lys	Lys	Thr	Pro	Glu	Lys	Lys	Thr	Gly	Asn	Lys
							145		150			155		160	

Asp	Cys	Lys	Ala	Asp	Ile	Ala	Phe	Leu	Ile	Asp	Gly	Ser	Phe	Asn	Ile
							165		170			175			

Gly	Gln	Arg	Arg	Phe	Asn	Leu	Gln	Lys	Asn	Phe	Val	Gly	Lys	Val	Ala
							180		185			190			

Leu	Met	Leu	Gly	Ile	Gly	Thr	Glu	Gly	Pro	His	Val	Gly	Leu	Val	Gln
							195		200			205			

Ala	Ser	Glu	His	Pro	Lys	Ile	Glu	Phe	Tyr	Leu	Lys	Asn	Phe	Thr	Ser
							210		215			220			

Ala	Lys	Asp	Val	Leu	Phe	Ala	Ile	Lys	Glu	Val	Gly	Phe	Arg	Gly	Gly
							225		230			235		240	

Asn	Ser	Asn	Thr	Gly	Lys	Ala	Leu	Lys	His	Thr	Ala	Gln	Lys	Phe	Phe
							245		250			255			

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
260 . 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
 275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
 340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
355 360 . . . 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
370 375 . . . 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
 385 . . . 390 . . . 395 . . . 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
450 455 460 .

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
515 520 525

Phe Leu Glu Ser Gln Gln
545 550

<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228
tggtctcgca caccgatc

18

<210> 229
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229
ctgcgtgtcca caggggag

18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230
ccttgaagca tactgctc

18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231
gagatagcaa tttccgccc

18

<210> 232

<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 232
ttcctcaaga gggcagcc 18

<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 233
cttggcacca atgtccgaga ttcc 24

<210> 234
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 234
gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235
<211> 2586
<212> DNA
<213> Homo sapiens

<400> 235
ccggcgctc ccgcacccgc ggcccccca cccgcgcgt cccgcacatcg caccgcagc 60
ccggcgccct cccggcgaaa gcgagcagat ccagtccggc cccgcagcgc aactcggtcca 120
gtcggggcgg cgctgcggg cgcaagacgg agatgcagcg gcttggggcc accctgtgt 180
gcctgtgtct ggccggcgccg gtccccacgg ccccccgcgc cgctccgcacg ggcacctcg 240
ctccagtc aa gcccccccg gctctcagct accccgcaggaa ggaggccacc ctcaatgaga 300
tgttccgcga gtttggggaa ctgatggagg acacgcagca caaattgcgc agcgcgggtgg 360
aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420
tacctccag ctatcacaat gagaccaaca cagacacgaa ggttggaaat aataccatcc 480
atgtgcaccc agaaattcac aagataacca acaaccagac tggacaaatg gtctttcag 540
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acgaggactg tggcccgacg atgtactgcc agtttgccag cttccagtag acctgcccagc 660
catgccccggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

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aaaaaaaaa 2586

<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50. 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
 85 90 95
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
 100 105 110
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
 115 120 125
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
 130 135 140
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
 145 150 155 160
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
 165 170 175
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
 180 185 190
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 195 200 205
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
 210 215 220
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 245 250 255
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
 305 310 315 320
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 325 330 335
 Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
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<223> Synthetic oligonucleotide probe	
<400> 237	
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<400> 238	
ggaggactgt gccaccatga gagactcttc aaaccgaagg caaaattgg	49
<210> 239	
<211> 24	
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<223> Synthetic Oligonucleotide Probe	
<400> 239	
gcagagcgga gatgcagcgg cttg	24
<210> 240	
<211> 18	
<212> DNA	
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<223> Synthetic Oligonucleotide Probe	
<400> 240	
ttggcagtt catggagg	18
<210> 241	
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<223> Synthetic Oligonucleotide Probe	
<400> 241	
cctggcaaa aatgcaac	18

<210> 242
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 242
 ctccagctcc tggcgcacct cctc

24

<210> 243
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 243
 ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg

45

<210> 244
 <211> 3679
 <212> DNA
 <213> Homo Sapien

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 tctctctggg ctcagaagga ctctgaagat aacaataatt tcagccccatc 100
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 cacacataca ctttcctctc cttcaactgaa gactcacagt cactcactct 200
 gtgagcaggt catagaaaag gacactaaag ctttaaggac aggccctggcc 250
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gtgtagaatg actgccctgg gagggtggtt cttggggccc tggcagggtt 800
gctgaccctt accctgaaa acacaaagag caggactcca gactctcctt 850
gtgaatggtc ccctgcccctg cagctccacc atgaggttc tcgtggcccc 900
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atgtgtcacc tcccccaacc cgattcactc ttttctcctg ttttgtaaaa 3650
aataaaaaata aataataaca ataaaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Ala Thr Ala Thr Val Pro Val Val Pro Trp His Val Pro Cys Pro
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Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser
35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu
50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu
65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly
80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe
95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu
110 115 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His
125 . 130 135

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His
140 145 150

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser
 155 160 165
 Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile
 170 175 180
 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met
 185 190 195
 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg
 200 205 210
 Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu
 215 220 225
 Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu
 230 235 240
 Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg
 245 250 255
 Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys
 260 265 270
 Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu
 275 280 285
 His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser
 290 295 300
 Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu
 305 310 315
 Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala
 320 325 330
 Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn
 335 340 345
 Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn
 350 355 360
 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys
 365 370 375
 Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile
 380 385 390
 Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg
 395 400 405
 Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys

410	415	420
Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val		
425	430	435
Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu		
440	445	450
Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr		
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
530	535	540
Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
545	550	555
Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
560	565	570
Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr		
575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
590	595	600
Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
605	610	615
Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly		
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
 680 685 690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu
 695 700 705

Leu Pro Pro Leu Ser Gln Asn Ser
 710

<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgccatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaaccttgtcg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

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aggaggggga cattgtgtac cgccctctaca tgcggcagac catcatcaag 100

gtgatcaagt tcatcctcat catctgctac accgtctact acgtgcacaa 150

catcaaggta gacgtggact gcaccgtgga cattgagagc ctgacgggct 200
accgcaccta ccgctgtgcc cacccccctgg ccacacttta caagatcctg 250
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a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
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Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
20														30

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
35														45

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
50														60

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
65														75

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
80														90

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro 110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu 125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp 140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu 155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp 170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val 185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu 200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala 215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp 230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu 245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr 260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu 275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp 290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr 305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr 320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser 335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn 350	355	360

Asn Leu Lys Thr Ile Glu Glu Ile Ser Phe Gln His Leu His		
365	370	375
Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile		
380	385	390
Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu		
395	400	405
Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys		
410	415	420
Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe		
425	430	435
Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala		
440	445	450
Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln		
455	460	465
Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln		
470	475	480
Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile		
485	490	495
Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly		
500	505	510
Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp		
515	520	525
Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg		
530	535	540
Ala Asp Lys Glu Gln Ala		
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<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

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<210> 252

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 252
gatggctagg ttctggaggt tctg 24

<210> 253
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 253
caacctgcag gagattgacc tcaaggacaa caacctaag accatcg 47

<210> 254
<211> 1650
<212> DNA
<213> Homo Sapien

<400> 254
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gcgcctctccc gtccccggc gtttgctgct gctgccgctg ctgctggcc 100
tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200
ttatgccacc aactcctgca agaacttctc agaactgccc ctggcatgt 250
ggcttcaggc cggtccaggc gtttctagca ctggatttgg aaacttttag 300
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ccaggctgcc agtctcctat ttgtggataa tcccgtggc actgggttca 400
gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggt 450
tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500
ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550
cagctggcat tggtctagag ctttataagg ccattcagcg agggaccatc 600
aagtgcact ttgcgggggt tgccttgggt gattcctgga tctccctgt 650
tgattcggtg ctctcctggg gaccttacct gtacagcatg tctttctcg 700

aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750
gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800
agaaaatgatc attgaacaga acacagatgg ggtgaacttc tataacatct 850
taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900
cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950
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gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150
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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

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Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp
20 25 30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val
 35 40 45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn
 50 55 60
 Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
 65 70 75
 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu
 80 85 90
 Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp
 95 100 105
 Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr
 110 115 120
 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu
 125 130 135
 Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
 140 145 150
 Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
 155 160 165
 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
 170 175 180
 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
 185 190 195
 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
 200 205 210
 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
 215 220 225
 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 230 235 240
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys
 245 250 255
 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr
 260 265 270
 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser
 275 280 285
 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His
 290 295 300
 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln		
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca cggctggca 250

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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

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Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20													30
----	--	--	--	--	--	--	--	--	--	--	--	--	----

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
						35				40				45

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
							50			55				60

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
					65				70					75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
							80		85					90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
 95 100 105
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
 275 280 285
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
 290 295 300
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
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<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

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cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200
aatgtggaa agactctcg agctggtgca ggctgtgtcg gatcccagct 250
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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln
1	5	10	15

Ser	Gly	Lys	Cys
Ser	Tyr	Ser	Pro

Pro	Glu	Pro	Asp
Gln	Arg	Arg	Thr

2000-09-09 09:20:00

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35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly
 290 295 300
 Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser
 305 310 315
 Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp
 320 325 330
 Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met
 335 340 345
 Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp
 350 355 360
 Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg
 365 370 375
 Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly
 380 385 390
 Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp
 395 400 405
 Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser
 410 415 420
 Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Pro His
 425 430 435
 Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro
 440 445 450
 Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg
 455 460 465
 Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val
 470 475 480
 Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser
 485 490 495
 Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln
 500 505 510
 His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser
 515 520 525
 Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro
 530 535 540
 Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu
 545 550 555

Cys

<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien

<400> 260
gcccgcgcgt ctctccggc gcccacacct gtctgagcgg cgcagcgagc 50
cgccggccgg gcgggctgct cggcgccgaa cagtgcgtgg catggcagg 100
atcccaggc tcctcttcct tcttttctt ctgctctgtg ctgttggca 150
agtgagccct tacagtgccc cctggaaacc cacttggcct gcataccgcc 200
tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300
taagggact ccactgcca cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcattc 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcagg 500
tcagcattt tgggaaggac ttccctgctca actaccctt ctaacatca 550
gtgaagttat ccacggctg caccggcacc ctgggtggcag agaagcatgt 600
cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgccc ttccctaaagc ccaagttaa agatgggtgt 700
cgaggggcca acgactccac ttcaagccatg cccgagcaga taaaattca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaaggcga 800
atgccaatga catcgccatg gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ttccctgctaa 900
gcagctgcca gggggcagaa ttcaacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccagcca ggggcagcg ggtctgggt 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150
 gatttcaacg tggctgtcag aatcactcct ctcaaatacg cccagatttg 1200
 ctattggatt aaaggaaact acctggattt tagggagggg tgacacagtg 1250
 ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagagg 1300
 ccaaattgtt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350
 tgtgtgttaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400
 tgactggctt tactatttga aaactggttt gtgtatcata tcataatatca 1450
 tttaaggagt ttgaaggcat acttttgcatt agaaataaaa aaaatactga 1500
 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgttttg 1550
 caaactttga ttttatttc atctgaactt gtttcaaaga tttatattaa 1600
 atatttggca tacaagagat atgaaaaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu			
1	5	10	15

Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro			
20	25		30

Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr			
35	40		45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu			
50	55		60

Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu			
65	70		75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu			
80	85		90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile			
95	100		105

Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser			
110	115		120

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
 125 130 135
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
 140 145 150
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
 155 160 165
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
 170 175 180
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
 185 190 195
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
 200 205 210
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
 215 220 225
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
 230 235 240
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
 245 250 255
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
 260 265 270
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
 275 280 285
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
 290 295 300
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
 305 310 315
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
 320 325 330
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
 335 340 345
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
 350 355 360
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
 365 370 375
 Asn Tyr Leu Asp Cys Arg Glu Gly
 380

<210> 262
<211> 1378
<212> DNA
<213> Homo Sapien

<400> 262
gcacgcgcct gggctctcg agcctgctgc ctgctcccc gccccaccag 50
ccatgggttgt ttctggagcg ccccccagccc tgggtggggg ctgtctcgcc 100
accttcacct ccctgctgct gctggcgctcg acagccatcc tcaatgcggc 150
caggataacct gttcccccag cctgtggaa gccccagcag ctgaaccggg 200
ttgtggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
atccagaaga atgggaccca ccactgcgcga gggtctctgc tcaccagccg 300
ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
cggtcccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450
ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctcgagcgct 500
ccatacagtt ctcagagcgg gtcctgcccc tctgcctacc tgatgcctct 550
atccacccctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600
ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650
ttcctatcat cgactcgaa gtctgcagcc atctgtactg gcggggagca 700
ggacaggaccc ccatcactga ggacatgctg tgtgcggct acttggaggg 750
ggagcgggat gcttgtctgg gcgactccgg gggcccccctc atgtgccagg 800
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850
gccgagcgca acaggccccgg ggtctacatc agcctctctg cgcaccgctc 900
ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950
gggggtggggc cctcaggca ccgagccagg gctctggggc cgccgcgcgc 1000
tccttagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050
cacatctgga tctggatctg cggcgccctc gggcggttcc ccccgccgta 1100
aataggctca tctaccccta cctctggggg cccggacggc tgctgcggaa 1150

agggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200
 catcaggccc cgcccaacgg cctcatgtcc ccgcacccac gacttccggc 1250
 cccgcccccg ggccccagcg ctttgtgtta tataaatgtt aatgattttt 1300
 ataggttattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350
 ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263
 <211> 317
 <212> PRT
 <213> Homo Sapien.

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
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Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
		20							25				30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
			35						40			45		
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
	50							55				60		
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
	65						70					75		
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
	80						85					90		
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
	95						100					105		
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
	110						115					120		
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
	125					130						135		
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
	140						145					150		
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
	155						160					165		
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
	170						175					180		

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
 185 190 195

Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
 200 205 210

Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
 215 220 225

Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
 230 235 240

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
 245 250 255

Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
 260 265 270

Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
 275 280 285

Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
 290 295 300

Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
 305 310 315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 268
gggaaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatggac tccaaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gcctctatcc tctctggcaa atgcagttac agcccgagc ccgac 45

<210> 276

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 276

ggcaggat tccagggttc c 21

<210> 277

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 277

ggctatgaca gcagggttc 18

<210> 278

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 278

tgacaatgac cgaccagg 18

<210> 279

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 279

gcatcgatt gctggtagag caag 24

<210> 280

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280
ttacagtgcc ccctggaaac ccacttggcc tgcataaccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gtcataaca gttccattgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctggcg actccggggg cccccatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gttcctgat gttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggcccggtt gggccctcac 100

agatgaggag aaacgttga tggtagctc gcacaacctc taccgggccc 150
aggatatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250
caaggagcgc gggcgccgag gcgagaatct gttccatc acagacgagg 300
gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350
tacaacctca ggcggccac ctgcagccca ggccagatgt gcggccacta 400
cacgcaggta gtatggcca agacagagag gatcggctgt gttcccact 450
tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500
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gttaactgagg ccccatcattt ccggggcact gaagcatcag actctaggaa 700
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cagaggtctc aggctccctg gcaacccaagg ctctgcctgc tgtggaaacc 800
caggccccaa cttccttagc aacgaaagac ccgcctcca tggcaacaga 850
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gcctgcctc cttggatgag gagccagtta cttccccaa atcgaccat 950
gttcctatcc caaaaatcagc agacaaatgt acagacaaaa caaaaatgtcc 1000
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caagccttagc gttgtgtcag ggctgaactc gggccctggc catgtgtggg 1350
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 catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500
 ggccctccgg aaggaaagg ctacggggca tgtgcctcat cacaccatcc 1550
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600
 ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtccctg 1650
 ggggtgggag gatttgaggg agctcaactgc ctacctggcc tggggctgtc 1700
 tgcccacaca gcatgtgcgc tctccctgag tgccctgtta gctggggatg 1750
 gggattccta gggcagatg aaggacaagc cccactggag tggggttctt 1800
 tgagtggggg aggcaggac gagggaaagga aagtaactcc tgactctcca 1850
 ataaaaacct gtccaaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu
1								5				10		15

Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp
								20			25		30	

Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
								35			40		45	

Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
								50			55		60	

Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
								65			70		75	

Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Gly	Glu	Asn	Leu	Phe	
								80			85		90	

Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	
								95			100		105	

Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
								110			115		120	

Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
								125			130		135	

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
 140 145 150
 Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
 155 160 165
 Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
 170 175 180
 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
 185 190 195
 Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
 200 205 210
 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
 215 220 225
 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
 230 235 240
 Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
 245 250 255
 Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
 260 265 270
 Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
 275 280 285
 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
 290 295 300
 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
 305 310 315
 Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
 320 325 330
 Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
 335 340 345
 Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
 350 355 360
 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
 365 370 375
 Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
 380 385 390
 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
 395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

 Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435

 Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
 440 445 450

 Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

gtaactgaag tcaggcttt catttggaa gccccctcaa cagaattcgg 50

tcattctcca agttatggtg gacgtacttc tgggttctc cctctgctt 100
cttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150
caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaaactga 200
acaacaatga attggagacc attccaaatc tgggaccagt ctggcaaat 250
attacacttc tctccttggc tgaaaacagg attgtgaaa tactccctga 300
acatctgaaa gagttcagt cccttggaaac tttggacctt agcagcaaca 350
atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400
tatctcaaca gcaaccgagt cacatcaatg gaacctgggt atttgacaa 450
tttggccaac acactccttg tggtaaagct gaacaggaac cgaatctcag 500
ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattt 550
aaccgaaaca agattaaaaa tggatgtgg ctgacattcc aaggccttgg 600
tgctctgaag tctctgaaaa tggaaagaaa tggagtaacg aaacttatgg 650
atggagcttt ttggggctg agcaacatgg aaatttgca gctggaccat 700
aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750
gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800
cctggagtt ctggcagaag ctcagtgagc tggacctaac tttcaatcac 850
ttatcaaggt tagatgattc aagcttcctt ggcctaagct tactaaatac 900
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<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
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					20				25				30	

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu		
35	40	45
Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser		
50	55	60
Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu		
65	70	75
Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu		
80	85	90
Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro		
95	100	105
Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr		
110	115	120
Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu		
125	130	135
Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys		
140	145	150
Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn		
155	160	165
Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala		
170	175	180
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met		
185	190	195
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		
200	205	210
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
215	220	225
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
230	235	240
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		
245	250	255
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser		
260	265	270
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
275	280	285
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		

290	295	300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile 305	310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg 320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala 335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn 350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys 365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys 380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln 395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly 410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp 425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala 440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser 455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu 470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln 485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu 500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn 515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn 530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg 545	550	555

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 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
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 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
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 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
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 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
 665 670 675
 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
 680 685 690
 Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
 695 700 705
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 710 715 720
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
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 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
 740 745 750
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
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 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
 770 775 780
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 785 790 795
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 800 805 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 815 820 825
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 830 835 840
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 860 865 870
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 875 880 885
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 905 910 915
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 920 925 930
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 935 940 945
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
 950 955 960
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
 965 970 975
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
 980 985 990
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
 995 1000 1005
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
 1010 1015 1020
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
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 Asn Phe Gln Ser Tyr Asp Leu Asp Thr
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<210> 291

<211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
					20				25			30		

Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
					35				40			45		

Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
					50				55			60		

Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
					65				70			75		

Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
					80				85			90		

Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
					95				100			105		

Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
					110				115			120		

Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
					125				130			135		

Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
					140				145			150		

Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser
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Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly 170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly 185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg 200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp 215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln 230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile 245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val 260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp 275	280	285
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Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp 305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys 320	325	330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp 335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro 350	355	360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys 365	370	375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn 380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val 395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp 410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
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 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
 455 460 465
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
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 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
 485 490 495
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
 500 505 510
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
 515 520 525
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
 530 535 540
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
 545 550 555
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
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 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
 575 580 585
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
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 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn
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 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
 635 640

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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<213> Homo Sapien

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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
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Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
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Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
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Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
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Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
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Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
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Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
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Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
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Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
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Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
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Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
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Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
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 860 865 870
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 875 880 885
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 890 895 900
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 980 985 990
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1010

1015

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<223> Synthetic oligonucleotide probe

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<210> 310

<211> 3296

<212> DNA

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<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315			
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Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys			
35		40	45
Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys			
50		55	60
Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys			
65		70	75
Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu			
80		85	90
Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met			
95		100	105
Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met			
110		115	120
Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met			
125		130	135
Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg			
140		145	150
Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg			
155		160	165

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
 170 175 180
 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
 185 190 195
 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
 200 205 210
 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
 215 220 225
 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
 230 235 240
 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
 245 250 255
 Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
 260 265 270
 Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
 275 280 285
 Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro
 290 295 300
 Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr
 305 310 315
 Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro
 320 325 330
 Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
 335 340 345
 Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala
 350 355 360
 Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln
 365 370 375
 Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val
 380 385 390
 His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu
 395 400 405
 Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly
 410 415 420
 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425	430	435
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Ala Ala Arg Leu Val Leu Pro Leu Gly Arg	Leu Met His Ser Gly	
440	445	450

Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly	Leu His Ser	
455	460	465

Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480

Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495

Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg		
500	505	

<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 316

gatggttcct gctcaagtgc cctg 24

<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgtt aggaccacg tacg 24

<210> 318

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 318

ctgatggag gacctgtgt aatgtgctac aggaagagcc 50

<210> 319

<211> 2110

<212> DNA

<213> Homo Sapien

<400> 319

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catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200
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aaaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

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Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
35 40 45

His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
50 55 60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
 65 70 75
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
 80 85 90
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
 95 100 105
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
 110 115 120
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
 125 130 135
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
 140 145 150
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
 155 160 165
 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
 170 175 180
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
 185 190 195
 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
 200 205 210
 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
 215 220 225
 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
 230 235 240
 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
 245 250 255
 Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
 260 265 270
 Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
 275 280 285
 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
 290 295 300
 Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
 305 310 315
 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Asp His Pro Glu		
440	445	450
<210> 321		
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<400> 321		
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<212> DNA		
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<223> Synthetic Oligonucleotide Probe		
<400> 322		
cactgacagg gttcctcacc cagg 24		
<210> 323		
<211> 45		
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aatttatgc cccgtggtgc cctgcttgc aaaaatcttca 200

accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gaggcagccag gactgagtgg acggtttatac 300

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ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtgata 400

aagagtggaa gagtattgag cccgtttcat catggttgg tccaggttct 450

gttctgatga gtagtatgtc agcactctt cagctatcta tgtggatcag 500

gacgtgccat aactactta ttgaagacct tggattgcca gtgtgggat 550

catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600

ctctgtatga tatttggtgc agattgcctt tgcccttcaa aaaggcgcag 650

accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700

aacctttgaa aaaagtggag gaggaacaag aggccgatga agaagatgtt 750

tcagaagaag aagctgaaag taaagaagga acaaacaag actttccaca 800

gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850

cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900

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<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val
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Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn
									25					30

Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
									40					45

Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
									55					60

Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
									70					75

Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly
									85					90

Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His
									100					105

Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys
									115					120

Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile
									125					135

Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser
									140					150

Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys
									155					165

His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser
									170					180

Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu
									185					195

Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys
									200					210

Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu	Leu
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215 220 225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu

230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
245 250 255

Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
260 265 270

Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
275 280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

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<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330
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<220>
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<400> 330
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<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

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cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

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														30
			20							25				

Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Glu	Leu	Val	Gln	Ser	Leu	Lys
													45
			35						40				

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
														60
			50					55						

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
														75
			65					70						

Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
														90
			80					85						

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
														105
			95					100						

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
														120
			110					115						

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
														135
			125					130						

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
														150
			140					145						

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
														165
			155					160						

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
														180
			170					175						

Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
														195
			185					190						

Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Lys	Ser	Gln	Val	Leu	
														210
			200					205						

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg		
215	220	225
Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His		
230	235	240
Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu		
245	250	255
Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu		
260	265	270
Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro		
275	280	285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys		
290	295	300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His		
305	310	315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu		
320	325	330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met		
335	340	345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys		
350	355	360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr		
365	370	375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp		
380	385	390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile		
395	400	405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn		
410	415	420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg		
425	430	435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala		
440	445	450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr		
455	460	465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr		
470	475	480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
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<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta ct tg 24

<210> 337
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 337
ggcacatga ctgaccgtat ttatgcagag aaagagctgg tgcag 45

<210> 338
<211> 2789

<212> DNA
<213> Homo Sapien

<400> 338
gcagtattga gtttacttc ctccttttt tagtggaaaga cagaccataa 50
tcccaagtgtg agtggaaattt attgtttcat ttattaccgt tttggctggg 100
ggtagttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150
agacaggaca atcttcttgg ggtatgctggt cctggaaagcc agcgggcctt 200
gctctgtctt tggcctcatt gaccccaggt tctctggta aaactgaaag 250
cctactactg gcctggtgcc catcaatcca ttgatccttgg aggctgtgcc 300
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350
ttggctctgc tgccggccagc gcttcccctc atcttagggc tgtctctggg 400
gtcgccgcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450
atccctgtgt cgaggctgtt ggggagcgag gagggccaca gaatccagat 500
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cccctactac agggacccca acaagcccta caagaagggtt ctcaggactc 600
ggtacatcca gacagagctg ggctccctg agcggttgct ggtggctgtc 650
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aactctacca ccgctgccgc ctcagcaacc tggaggggct agggggccgt 2600
gcccagctgg ctatggctct cttttagcag gagcaggcca atagcactta 2650
gcccgcctgg gggccctaac ctcattacct ttccttgtc tgcctcagcc 2700
ccaggaaggg caaggcaaga tggtgacag atagagaatt gttgctgtat 2750
tttttaata taaaaatgtt attaaacatg tcttcgtcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro
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Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg
20 25 30

Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala
35 40 45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
50 55 60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
65 70 75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val	
110	115	120
Asn Arg Thr Val Ala His His Phe Pro	Arg Leu Leu Tyr Phe Thr	
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala	Gly Met Gln Val Val Ser	
140	145	150
His Gly Asp Glu Arg Pro Ala Trp	Leu Met Ser Glu Thr Leu Arg	
155	160	165
His Leu His Thr His Phe Gly Ala Asp	Tyr Asp Trp Phe Phe Ile	
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala	Pro Arg Leu Ala Ala Leu	
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala	
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala	Arg Tyr Cys His Gly	
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg	
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro	
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser	Leu Gly Val Gly	
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln	Tyr Arg Ser Phe Glu Leu	
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly	Ser Ser Ala Phe Leu	
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser	Glu Gly Thr Leu Met Tyr	
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu	Leu Glu Arg Ala Tyr	
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln	Ile Arg Asn Leu Thr Val	
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser	Trp Pro Val Gly Leu	
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp
 365 370 375
 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala
 380 385 390
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp
 395 400 405
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro
 410 415 420
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg
 425 430 435
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu
 440 445 450
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg
 455 460 465
 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met
 470 475 480
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu
 485 490 495
 Leu Val Ala Glu Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe
 500 505 510
 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
 515 520 525
 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
 530 535 540
 Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg
 545 550 555
 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
 560 565 570
 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
 575 580 585
 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
 590 595 600
 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
 605 610 615
 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
 620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
 635 640 645
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
 650 655 660
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
 665 670 675
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
 680 685 690
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
 695 700 705
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
 710 715 720
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
 725 730 735
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
 740 745 750
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
 755 760 765
 Gln Glu Gln Ala Asn Ser Thr
 770

<210> 340
 <211> 1572
 <212> DNA
 <213> Homo Sapien

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 tgtccccaaag ccgttctaga cgcggaaaaa atgcttctg aaagcagctc 100
 cttttgaag ggtgtatgc ttgaaagcat tttctgtgct ttgatcacta 150
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
 catcatcacc tacaagctcc taacaaagaa gatatctga aaatttcaga 250
 ggatgagcgc atggagctca gtaagagctt tcgagttatac tgtattatcc 300
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
 accaaacact gtgacaaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtggta atgatgagaa 450
aagcttacaa atacgcctt gataagtata gagaccaata caactggtc 500
ttccttgcac gccccactac gtttgcatac attgaaaacc taaagtattt 550
tttgttaaaa aaggatccat cacagcctt ctatctaggc cacactataa 600
aatctggaga ctttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700
tcctgaacag ggagggatga ttggaaagat atctgaagat aaacagctag 750
cagtttgcct gaaatatgct ggagtattt cagaaaatgc agaagatgct 800
gatggaaaag atgtatttaa taccaaattct gttggcctt ctattaaaga 850
ggcaatgact tattttttttt accaggtgtt agaaggctgt tggtcagata 900
tggctgttac ttttaatggc ctgactccaa atcagatgca tgtgtatgt 950
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gtaactacat atccaataaca gctgtatgtt tcttttctt ttcttaattt 1150
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gggtggttttt tttttttaaa acacatgaac attgtaaatg tggtggaaag 1250
aagtgtttta agaataataa ttttgc当地 aaactattaa taaatattat 1300
atgtataaaa ttcttaattt tgaacattag aaatctgtgg ggcacatatt 1350
tttgctgatt ggtttttttt ttttaacagg tcttttagcgt tctaagat 1400
gcaaatgata tctctagttg tgaatttgc当地 attaaagtaa aacttttagc 1450
tgtgtgtcc ct当地acttct aatactgatt tatgttctaa gc当地ccccaa 1500
gttccaaatgg atttgccttc tcaaaaatgta caactaagca actaaagaaa 1550
attaaagtga aagttgaaaa at 1572

<210> 341
<211> 318
<212> PRT
<213> Homo Sapien

<400> 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly
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Ser Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile														
	20							25					30	
Gly His Gly Asn Arg Met His His His Glu His His His Leu Gln														
	35							40					45	
Ala Pro Asn Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg														
	50							55					60	
Met Glu Leu Ser Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val														
	65							70					75	
Lys Pro Lys Asp Val Ser Leu Trp Ala Ala Val Lys Glu Thr Trp														
	80							85					90	
Thr Lys His Cys Asp Lys Ala Glu Phe Phe Ser Ser Glu Asn Val														
	95							100					105	
Lys Val Phe Glu Ser Ile Asn Met Asp Thr Asn Asp Met Trp Leu														
	110							115					120	
Met Met Arg Lys Ala Tyr Lys Tyr Ala Phe Asp Lys Tyr Arg Asp														
	125							130					135	
Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr Thr Phe Ala Ile														
	140							145					150	
Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp Pro Ser Gln														
	155							160					165	
Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu Glu Tyr.														
	170							175					180	
Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met Lys														
	185							190					195	
Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln														
	200							205					210	
Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val														
	215							220					225	
Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala														
	230							235					240	
Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile														
	245							250					255	
Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys														

260

265

270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
275 280 285
Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly
290 295 300
His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser
305 310 315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttcttagacg cg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

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<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345
gggtgtatg cttggaaagca ttttctgtgc tttgatcact atgcttaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346
gggatgcagg tggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347
ccctcatgtt ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaat acgactcact ataggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaaggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 350
ggattctaat acgactcact atagggcgcc gatgtccact ggggctac 48

<210> 351
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 351
ctatgaaatt aaccctcact aaagggacga ggaagatggg cggatgg 48

<210> 352
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 352
ggattctaat acgactcact atagggcacc cacgcgtccg gctgatt 47

<210> 353
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 353
ctatgaaatt aaccctcact aaagggacgg gggacaccac ggaccaga 48

<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 354
ggattctaat acgactcact atagggcttg ctgcggttt tggccctg 48

<210> 355
<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 355

ctatgaaatt aaccctcact aaagggagct gccgatccca ctggatt 48

<210> 356

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 356

ggattctaat acgactcact atagggcgga tcctggccgg cctctg 46

<210> 357

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 357

ctatgaaatt aaccctcact aaagggagcc cggcatggg ctcagtta 48

<210> 358

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 358

ggattctaat acgactcact atagggcgga aagatggcga ggaggag 47

<210> 359

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 359

ctatgaaatt aaccctcact aaagggacca aggccacaaa cgaaaaatc 48

<210> 360
<211> 48
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 360
ggattctaat acgactcact atagggctgt gctttcattc tgccagta 48

<210> 361
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 361
ctatgaaatt aaccctcact aaagggaggg tacaattaag gggtagat 48

<210> 362
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 362
ggattctaat acgactcact atagggccccg cctcgctcct gctcctg 47

<210> 363
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 363
ctatgaaatt aaccctcact aaagggagga ttgccgcgac cctcacag 48

<210> 364
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 364

ggattctaat acgactcact atagggcccc tcctgccttc cctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 365

ctatgaaatt aaccctcact aaaggagtg gtggccgcga ttatctgc 48

<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

ggattctaat acgactcact atagggcgca gcgatggcag cgatgagg 48

<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 367

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gaactggaa tattttcaat ccagctgcta cttctttct actgacacca 400

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gtggttatca actcacagga ggagcaggaa ttcccttcct acaagaaaacc 500

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agtggcaatg ggtggacggc acaccttga caaagtctct gagttctgg 600

gatgttagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650

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 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 997

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<211> 219

<212> PRT

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Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
					35				40					45

Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
					50			55						60

Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser
					65				70					75

Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser
					80				85					90

Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
					95				100					105

Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
					110				115					120

Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg
					125				130					135

Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
					140				145					150

Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
					155				160					165

Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
					170				175					180

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu
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<213> Artificial Sequence

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<400> 378

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<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 380

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<210> 381

<211> 26

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 381

gcagatttg aggacagcca cctcca 26

<210> 382
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ggccttgcag acaaccgt 18

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catcaāgcgc ctctacca 18

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ggccatcac agtccct 18

<210> 388

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ggatgttgtt gaacacagaa ca 22

<210> 389

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<400> 389

tgcaggctgc atgctgccag tt 22

<210> 390

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<220>

<223> Synthetic oligonucleotide probe

<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

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<210> 393

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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atgcctcca tgcccacg 20

<210> 394

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ccaggagagc tggcgatg 18

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ggcagagact tccagtact ga 22

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<400> 403
gccaagggtg gtgttagata gg 22

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caggccccct tgatctgtac ccca 24

<210> 405
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<210> 407
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<400> 411
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<210> 412
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<400> 412
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gggccctaac ctcattacct tt 22

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<400> 421
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<211> 310

<212> PRT

<213> Homo Sapien

<400> 423

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				20				25				30	

Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
				35				40				45		

Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
				50				55				60		

Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Ile	Gln	Asp	Glu	Gln	Thr
				65				70				75	

Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly
				80				85				90		

Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val
				95				100				105		

Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg
					110			115				120		

Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val
				125				130				135		

Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
				140				145				150		

Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly
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His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu
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Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe
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His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
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Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
215 220 225
Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
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Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
245 250 255
Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
260 265 270
Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
275 280 285
Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
290 295 300
Asp Phe Arg His Lys Ser Ser Phe Val Ile
305 310